



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 137287**

**TO: Jeffrey Parkin**  
**Location: rem/3d39/3c18**  
**Art Unit: 1648**  
**Sunday, November 14, 2004**

**Case Serial Number: 09/687864**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Examiner Parkin,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

137287

me

From: Parkin, Jeffrey  
Sent: Saturday, November 06, 2004 4:58 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence Search for U.S. Serial No. 09/687,864

11/06/04  
11:00 AM  
STIC-BIOTECH/CHEMLIB

Please search SEQ ID NOS.: 12, 13, 15, 17, and 19 from U.S. Serial No. 09/687,864 v. all relevant databases, including interference. Place results on both disk and paper. Thanks!

JSP  
AU 1648  
REM 3D39  
2-0908

[http://expoweb1:8001/cgi-bin/expo/GenInfo/snquery.pl?APPL\\_ID=09687864](http://expoweb1:8001/cgi-bin/expo/GenInfo/snquery.pl?APPL_ID=09687864).

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 6472.4 Seconds  
(without alignments)  
16453.933 Million cell updates/sec

Title: US-09-687-864A-12  
Perfect score: 2252  
Sequence: 1 aagcttgccgcatgctgta.....ctcgagtgaataatctagata 2252

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1470.2	65.3	10000	14 AF0383398	AF0383398 Simian-Hu
2	1452.6	64.5	2046	6 CQ753919	CQ753919 Sequence
3	1452.6	64.5	2610	6 CQ753921	CQ753921 Sequence
4	1452.6	64.5	9860	14 AF217181	AF217181 Simian-Hu
5	1452.6	64.5	9860	14 SIU89134	U89134 Simian-Hu
6	1452.6	64.5	10501	6 BD161892	BD161892 Nonhuman
7	1448	64.3	9713	14 HIVI039362	U39362 Human immun
8	1338.6	59.4	2010	6 CQ753923	CQ753923 Sequence
9	1338.6	59.4	2574	6 CQ753925	CQ753925 Sequence
10	1262	56.0	2553	14 AY247221	AY247221 HIV-1 iso
11	1241.4	55.1	2568	14 AY426111	AY426111 HIV-1 clo
12	1239.8	55.1	2568	14 AY426112	AY426112 HIV-1 clo
13	1238.2	55.0	2568	14 AY426118	AY426118 HIV-1 clo
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20	1226.8	54.5	3061	14 HIVENVBALA	M63929 Human immun
21	1225.2	54.4	3807	6 AR034235	AR034235 Sequence
22	1225.2	54.4	3807	6 I12144	I12144 Sequence 5
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24	1225.2	54.4	3808	14 HIVBAL1A	M68893 Human immun
25	1224	54.4	2559	14 AY669732	AY669732 HIV-1 iso
26	1223.8	54.3	2547	14 AY426125	AY426125 HIV-1 iso
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28	1222.2	54.3	2544	14 AY669726	AY669726 HIV-1 iso
29	1222.2	54.3	2547	14 AY426126	AY426126 HIV-1 clo
30	1222.2	54.3	9540	14 HIVJRC5F	M38429 Human immun
31	1221.6	54.2	2568	14 AY247225	AY247225 HIV-1 iso
32	1219	54.1	3211	14 HIVU45960	U45960 Human immun
33	1208.2	53.7	2552	6 I05789	I05789 Sequence 8
34	1207.4	53.6	2559	14 AF025750	AF025750 HIV-1 iso
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38	1197	53.2	1512	6 AX153805	AX153805 Sequence
39	1197	53.2	1512	6 BD017695	BD017695 Assay met
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41	1196.8	53.1	9074	14 HIVU43096	U43096 Human immun
42	1196	53.1	4273	14 HIVSC	M17450 Human immun
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44	1195.2	53.1	2565	14 AF025754	AF025754 HIV-1 iso
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ALIGNMENTS

RESULT 1	AF038398	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome.	10000 bp	DNA	linear	VRL 02-FEB-1998
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DEFINITION	AF038398	AF038398.1	GI:2828036				
ACCESSION	AF038398	AF038398.1	GI:2828036				
VERSION	AF038398	AF038398.1	GI:2828036				
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ORGANISM	AF038398	AF038398.1	GI:2828036				
REFERENCE	AF038398	AF038398.1	GI:2828036				
AUTHORS	AF038398	AF038398.1	GI:2828036				
TITLE	AF038398	AF038398.1	GI:2828036				
JOURNAL	AF038398	AF038398.1	GI:2828036				
MEDLINE	AF038398	AF038398.1	GI:2828036				
PUBMED	AF038398	AF038398.1	GI:2828036				
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AUTHORS	AF038398	AF038398.1	GI:2828036				
TITLE	AF038398	AF038398.1	GI:2828036				
JOURNAL	AF038398	AF038398.1	GI:2828036				
FEATURES	AF038398	AF038398.1	GI:2828036				
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LTR	AF038398	AF038398.1	GI:2828036				
repeat_region	AF038398	AF038398.1	GI:2828036				
misc_feature	AF038398	AF038398.1	GI:2828036				



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9307..9823					
/note="U3 region"					
repeat_region		9824..10000			
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ORIGIN					
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Best Local Similarity 98.8%; Pred. No. 1.6e-299;					
Matches 1481; Conservative 0; Mismatches 18; Indels 0; Gaps 0;					
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QY	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACTCTA	171		
Db	6435	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACTCTA	6494		
QY	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGGCCACACAT	231		
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QY	352	GATGAAAGCCTAAAGCCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCAC	411		
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QY	592	AAGTATAGTTAATAAGTTGTAACACCTCAGTCAATTACAGGCGCTGTCCAAGGTATCC	651		
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RESULT 2					
CQ753919					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match 64.5%; Score 1452.6; DB 6; Length 2046;					
Best Local Similarity 98.1%; Pred. No. 9.1e-296;					
Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;					
QY	52	TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111		
Db	37	TGGGGGTGGAGATGGGGCCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	96		
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QY 532 AAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT 591

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RESULT 3

CQ753921

LOCUS CQ753921 2610 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 26 from Patent WO2004001051.

ACCESSION CQ753921

VERSION CQ753921.1 GI:44845221

KEYWORDS .

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1

AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.

TITLE Recombinant measles viruses expressing epitopes of antigens of rna viruses - use for the preparation of vaccine compositions

JOURNAL Patent: WO 2004001051-A 26 31-DEC-2003;

INSTITUT PASTEUR (FR)

FEATURES

source

1. .2610

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/mol\_type="unassigned DNA"

/db\_xref="taxon:11676"

ORIGIN

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Best Local Similarity 98.1%; Pred. No. 9e-296;

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QY 112 AAATTGTGGTCAAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCACCTCTA 171

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QY 172 TTTTGTGCATCAGATGCTAAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

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QY 352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCAC 411

Db 337 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCAC 396







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DEFINITION Simian-Human immunodeficiency virus strain SHIV-89.6P, complete genome.  
ACCESSION U89134  
VERSION U89134.1 GI:2108163  
KEYWORDS  
SOURCE  
ORGANISM Simian-Human immunodeficiency virus  
Simian-Human immunodeficiency virus  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 9860)  
AUTHORS Karlsson,G.B., Halloran,M., Li,J., Park,I.W., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.  
TITLE Characterization of molecularly cloned simian-human immunodeficiency viruses causing rapid CD4+ lymphocyte depletion in rhesus monkeys  
JOURNAL J. Virol. 71 (6), 4218-4225 (1997)  
MEDLINE 97296224  
PUBMED 9151808  
REFERENCE 2 (bases 1 to 9860)  
AUTHORS Karlsson,G.B., Halloran,M., Li,J., Park,I., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.  
TITLE Direct Submision  
JOURNAL Submitted (10-FEB-1997) Human Retrovirology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA  
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VERSION			
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AUTHORS			
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JOURNAL			
COMMENT			
BD161892 10501 bp DNA linear PAT 17-JAN-2003			
Nonhuman primate model of acquired immunodeficiency syndrome.			
BD161892			
BD161892.1 GI:27867650			
JP 2002159296-A/1.			
Simian-Human immunodeficiency virus			
Simian-Human immunodeficiency virus			
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate			
lentivirus group.			
1 (bases 1 to 10501)			
Shinohara,K., Sakai,K. and Honda,M.			
Nonhuman primate model of acquired immunodeficiency syndrome			
Patent: JP 2002159296-A 1 04-JUN-2002;			
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE			
ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH			
OS Simian-human immunodeficiency virus			
PN JP 2002159296-A/1			
PD 04-JUN-2002			
PF 27-NOV-2000 JP 2000360274			
PI KATSUAKI SHINOHARA,KOJI SAKAI,MITSUO HONDA			
PC C12N15/09,A01K67/027,C12N7/00,C12N7/02,G01N33/15,G01N33/50//			
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CC vif			
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CC derived from HIV-1			
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CC rev			
CC vpu			
CC env			





ACCESSION U39362 M96155  
VERSION U39362.2 GI:9409797  
KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 5029)  
AUTHORS Collman,R.G. and Yoon,H.L.  
JOURNAL Unpublished  
REFERENCE 2 (bases 5030 to 9713)  
AUTHORS Kim,F.M., Kolson,D.L., Balliet,J.W., Srinivasan,A. and Collman,R.G.  
TITLE V3-independent determinants of macrophage tropism in a primary  
human immunodeficiency virus type 1 isolate  
J. Virol. 69 (3), 1755-1761 (1995)  
JOURNAL 95156606  
MEDLINE 7853514  
PUBMED  
REFERENCE 3 (bases 1 to 9713)  
AUTHORS Collman,R., Balliet,J.W., Gregory,S.A., Friedman,H., Kolson,D.L.,  
Nathanson,N. and Srinivasan,A.  
TITLE An infectious molecular clone of an unusual macrophage-tropic and  
highly cytopathic strain of human immunodeficiency virus type 1  
J. Virol. 66 (12), 7517-7521 (1992)  
JOURNAL 93059708  
MEDLINE 1433527  
PUBMED  
REMARK Describes the isolation of the full-length clone and virus strain  
89.6  
REFERENCE 4 (bases 1 to 9713)  
AUTHORS Collman,R.G.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-1995) Ronald G. Collman, Pulmonary & Critical  
Care Division, University of Pennsylvania, 522 Johnson Pavilion,  
3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA  
REFERENCE 5 (bases 1 to 9713)  
AUTHORS Collman,R.G.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-2000) Ronald G. Collman, Pulmonary & Critical  
Care Division, University of Pennsylvania, 522 Johnson Pavilion,  
3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA  
REMARK Sequence updated by submitter  
COMMENT On Jul 24, 2000 this sequence version replaced gi:1055029.  
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Db	6335	ATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTA 6394
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Qy	311	ACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCAT 370

Db	6515	ACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAAAGCCTAAAGCCAT 6574
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Qy	431	ATACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAGAAAAGGAGAAATAAAAAATT 490
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Qy	491	GCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAGAAAAAATAATGCACTTTTTA 550
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Db	6875	ATTATTGTGTCCCGGTGGTTCGATGCTAAAGTGTAAACAATAAGACATTCAATGGAT 6934
Qy	731	CAGGACCATGCACAAATGTACAGCACAGTACAATGTACATGGAATTAGGCCAGTGGTGT 790
Db	6935	CAGGACCATGCACAAATGTACAGCACAGTACAATGTACATGGAATTAGGCCAGTGGTGT 6994
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Db	6995	CAACTCAACTGCTGTTAAATGCGCAGTCTAGCAGAGAAGACATAGTAATTAGATCTGAAA 7054
Qy	851	ATTTACAGACAAATGCTAAAACCATATAATAGTACAGCTAAATGAATCTGTAGTAATTAAAT 910
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KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1  
AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.  
TITLE Recombinant measles viruses expressing epitopes of antigens of rna  
viruses - use for the preparation of vaccine compositions  
JOURNAL Patent: WO 2004001051-A 30 31-DEC-2003;  
INSTITUT PASTEUR (FR)  
FEATURES Location/Qualifiers  
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Best Local Similarity 94.3%; Pred. No. 9.7e-272;  
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DEFINITION complete cds.  
ACCESSION AY247221  
VERSION AY247221.1 GI:30794652  
KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 2553)  
AUTHORS Robbins,K.E., Lemey,P., Pybus,O.G., Jaffe,H.W., Youngpairoj,A.S., Brown,T.M., Salemi,M., Vandamme,A.M. and Kalish,M.L.  
TITLE U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains  
JOURNAL J. Virol. 77 (11), 6359-6366 (2003)  
MEDLINE 22628496  
PUBMED 12743293  
REFERENCE 2 (bases 1 to 2553)  
AUTHORS Robbins,K.E.  
TITLE Direct Submission







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1297 ATGTATGCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTA 1356  
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Db 1534 GTGGG 1538

RESULT 12  
AY426112  
LOCUS  
DEFINITION  
AY426112 2568 bp DNA linear VRL 28-JUN-2004  
HIV-1 clone BaL-1A isolate BaL from USA envelope glycoprotein (env)  
gene, complete cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Human immunodeficiency virus 1 (HIV-1)  
Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
1 (bases 1 to 2568)  
Pastore,C., Ramos,A. and Mosier,D.E.  
Intrinsic Obstacles to Human Immunodeficiency Virus Type 1  
Coreceptor Switching  
J. Virol. 78 (14), 7565-7574 (2004)  
JOURNAL  
PUBMED  
15220431  
REFERENCE  
2 (bases 1 to 2568)  
Pastore,C., Ramos,A. and Mosier,D.E.  
Direct Submission  
Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research  
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA  
Location/Qualifiers  
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ORIGIN  
Query Match 55.1%; Score 1239.8; DB 14; Length 2568;  
Best Local Similarity 90.0%; Pred. No. 6.6e-251;  
Matches 1354; Conservative 0; Mismatches 142; Indels 9; Gaps 2;  
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QY 112 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCACCTCTA 171  
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Qy	1006	GCACATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTACAACAGATAGTTATATAAA	1065
Db	997	GCACATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTAAATAAGATAGTTATATAAA	1056
Qy	1066	TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGACCCA	1125
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Qy	1126	GAAATTTGAATGCACAGTTTTTAATGTGGAGGGGAATTTCTTACTGTAATACAGCACAA	1185
Db	1117	GAAATTTGTGACGCACAGTTTTTAATGTGGAGGGGAATTTTCTACTGTAATTCAACACAA	1176
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Db	1177	CTGTTTAAATAGTACTTGGAAATGTTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACACA	1236
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Qy	1366	CTAACAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGA	1425
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Qy	1426	GGAGATATGAGGGACAAATTTGGAGAACTGAATTATATAAATATAAAAGTAGTAAGAATTGAA	1485
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Qy	1546	GGAGG 1550	
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RESULT 13	AY426118	2568 bp	DNA	linear	VRL 28-JUN-2004
LOCUS	HIV-1 clone BaL-4p isolate BaL from USA	envelope glycoprotein (env)			
DEFINITION	gene, complete cds.				
ACCESSION	AY426118				
VERSION	AY426118.1	GI:37962981			
KEYWORDS					
SOURCE	Human immunodeficiency virus 1 (HIV-1)				
ORGANISM	Human immunodeficiency virus 1				
REFERENCE	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate				
AUTHORS	lentivirus group.				
TITLE	1 (bases 1 to 2568)				
JOURNAL	Pastore,C., Ramos,A. and Mosier,D.E.				
PUBMED	Intrinsic Obstacles to Human Immunodeficiency Virus Type 1				
REFERENCE	Coreceptor Switching				
AUTHORS	J. Virol. 78 (14), 7565-7574 (2004)				
TITLE	Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research				
JOURNAL	Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA				
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	Query Match	55.0%;	Score 1238.2; DB 14; Length 2568;
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Qy	52	TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	37	TGGGGGTGGAGATGGGGACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	96
Qy	112	AAATGTGGGTACAGTCTAATATATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTA	171
Db	97	AAATGTGGGTACAGTCTAATATATGGGGTACCTGTGTGGAAAGAACCAACCACCTCTA	156
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Qy	526	GTAAGAAAGAATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATACTAAT	585
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Db 1534 GTGGG 1538

RESULT 14

AY426110

LOCUS AY426110 2568 bp DNA linear VRL 28-JUN-2004

DEFINITION HIV-1 isolate BaL from USA envelope glycoprotein (env) gene, complete cds.

ACCESSION AY426110

VERSION AY426110.1 GI:37962965

KEYWORDS Human immunodeficiency virus 1 (HIV-1)

SOURCE

ORGANISM Human immunodeficiency virus 1

REFERENCE 1 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching

JOURNAL J. Virol. 78 (14), 7565-7574 (2004)

PUBMED 15220431

REFERENCE 2 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

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/proviral

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ORIGIN

Query Match 54.9%; Score 1236.6; DB 14; Length 2568;

Best Local Similarity 89.8%; Pred. No. 3.1e-250;

Matches 1352; Conservative 0; Mismatches 144; Indels 9; Gaps 2;

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Db 37 TGGGGGTGGAGATGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTCTACAGAA 96

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Qy 1366 CTAACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGA 1425

Db 1357 TTAACAAGAGATGGTGG--TCCAGAGGACAAACAAGACCGAGGTCTTCAGACCTGGAGGA 1413

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Db 1414 GGAGATATGAGGGACAAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAA 1473

Qy 1486 CCAATAGGAGTAGCACCCACCAGGGCCAAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGGG 1545

Db 1474 CCATTAGGAGTAGCACCCACCAGGCAAGAGAGAGAGAGTGGTGCAGAGAGAAAAAGAGCA 1533

Qy 1546 GGAGG 1550

Db 1534 GTGGG 1538

RESULT 15

AY426113

LOCUS

DEFINITION HIV-1 clone BaL-1B isolate BaL from USA envelope glycoprotein (env) gene, complete cds.

ACCESSION AY426113

VERSION AY426113.1 GI:37962971

KEYWORDS

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching

JOURNAL J. Virol. 78 (14), 7565-7574 (2004)

PUBMED 15220431

REFERENCE 2 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 54.9%; Score 1236.6; DB 14; Length 2568;

Best Local Similarity 89.8%; Pred. No. 3.1e-250;

Matches 1352; Conservative 0; Mismatches 144; Indels 9; Gaps 2;



Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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10: Geneseqn2003cs: \*  
11: Geneseqn2003ds: \*  
12: Geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19	1197	53.2	1512	5	AAF87100 HIV-1 gp1
20	1179.8	52.4	1422	12	ADP74731 iso
21	1173.4	52.1	4527	2	AAT33899 HIV-1 SF3

C	22	1172.6	52.1	3808	2	AAV58244	Aav58244 Insert re
C	23	1172.6	52.1	3808	2	AAV60252	Aav60252 Insert re
	24	1172.4	52.1	2571	2	AAT09010	Aat09010 HIV-1 str
	25	1172.4	52.1	2571	2	AAZ08741	Aaz08741 HIV-1 MN
	26	1172.4	52.1	2571	3	AAA93973	Aaa93973 Human imm
	27	1172.4	52.1	2571	4	AAC86877	Aac86877 Nucleotid
	28	1172.4	52.1	2571	5	AAH43700	Aah43700 Wild type
	29	1172.4	52.1	2571	8	ABX14499	Abx14499 Human imm
	30	1172.4	52.1	2571	9	ADA50072	Ada50072 Human imm
	31	1172.4	52.1	2571	10	AD81077	Ade81077 HIV-1 (MN
	32	1172.4	52.1	2571	12	ADG92081	Adg92081 HIV rev/e
C	33	1172.4	52.1	6474	2	AAQ40300	Aaq40300 Sequence
C	34	1172.4	52.1	6474	3	AAA89877	Aaa89877 Plasmid p
C	35	1172.4	52.1	6474	4	AA12795	Aas12795 Plasmid p
	36	1172.4	52.1	6926	2	AAQ40281	Aaq40281 Sequence
	37	1172.4	52.1	6926	3	AAA89880	Aaa89880 pP2-gp 16
	38	1172.4	52.1	6926	4	AA12798	Aas12798 Plasmid p
	39	1172.4	52.1	9738	2	AAx04765	Aax04765 The compl
	40	1172.4	52.1	9739	2	AAT58549	Aat58549 Human Imm
	41	1172.4	52.1	9745	2	AAx04766	Aax04766 The compl
	42	1172.4	52.1	9746	2	AAQ14752	Aaq14752 HIV-1 (MN-
	43	1172.4	52.1	9746	2	AAT58550	Aat58550 Human Imm
	44	1171.8	52.0	2553	2	AAQ76018	Aaq76018 DNA encod
	45	1168.6	51.9	1532	2	AAQ73687	Aaq73687 HIV virus

ALIGNMENTS

RESULT 1  
AAF82928  
ID AAF82928 standard; cDNA; 2252 BP.  
XX

AC AAF82928;

XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)

XX  
DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Homo sapiens.

Key	Location/Qualifiers
CDS	13..2252
sig_peptide	/*tag= a
	13..72
	/*tag= b
misc_feature	/note= "synthetic secretory signal peptide"
	73..1542
	/*tag= c
misc_feature	/note= "HIV-1 gp120 domain coding sequence"
	1543..1593
	/*tag= d
misc_feature	/note= "[Gly4Ser]3 linker coding sequence"
	1594..2252
	/*tag= e
	/note= "human CD154 long form extracellular domain coding sequence"

WO200126608-A2.

19-APR-2001.

13-OCT-2000; 2000WO-US028414.

14-OCT-1999; 99US-0159690P.

(LEDB/) LEDBETTER J A.



Db 1741 GATATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGT 1800

Qy 1801 GATCAGAAATCCTCAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCT 1860

Db 1801 GATCAGAAATCCTCAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCT 1860

Qy 1861 GTGTTACAGTGGGCTGAAAAAGGATACACACCATGAGCAACAACACTTGGTAACCCCTGGAA 1920

Db 1861 GTGTTACAGTGGGCTGAAAAAGGATACACACCATGAGCAACAACACTTGGTAACCCCTGGAA 1920

Qy 1921 AATGGGAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980

Db 1921 AATGGGAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980

Qy 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAG 2040

Db 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAG 2040

Qy 2041 TCCCCCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 2100

Db 2041 TCCCCCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 2100

Qy 2101 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCG 2160

Db 2101 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCG 2160

Qy 2161 GTGTTTGTCAATGTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCACGTCCTTT 2220

Db 2161 GTGTTTGTCAATGTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCACGTCCTTT 2220

Qy 2221 GGCTTACTCAAACTCGAGTGATAATCTAGATA 2252

Db 2221 GGCTTACTCAAACTCGAGTGATAATCTAGATA 2252

RESULT 2

AAF82929

ID AAF82929 standard; cDNA; 2209 BP.

AC AAF82929;

XX

DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX

DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.

XX

KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX

OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..2209

FT /\*tag= a

FT sig\_peptide 13..72

FT /\*tag= b

FT /note= "synthetic secretory signal peptide"

FT 73..1542

FT /\*tag= c

FT /note= "HIV-1 gp120 domain coding sequence"

FT 1543..1551

FT /\*tag= d

FT /note= "proAspPro linker coding sequence"

FT 1552..2209

FT /\*tag= e

FT /note= "human CD154 long form extracellular domain coding sequence"

XX

PN WO200126608-A2.

XX

PD 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028414.

PF

XX 14-OCT-1999; 99US-0159690P.

PR

XX (LEDB/) LEDBETTER J A.

PA (HAYD/) HAYDEN-LEDBETTER M S.

XX

PI Ledbetter JA, Hayden-Ledbetter MS;

XX

DR WPI; 2001-281790/29.

DR P-PSDB; AAB62334.

XX

PT DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PT

XX Example 1; Fig 3A; 55pp; English.

PS

XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 long form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)

CC

XX

SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;

Query Match 95.6%; Score 2153.8; DB 4; Length 2209;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 2207; Conservative 0; Mismatches 2; Indels 42; Gaps 1;

Qy 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Db 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Qy 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGG 120

Qy 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCCTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCCTCTATTTTGTGCA 180

Qy 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACATGCCTGTGTA 240

Db 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACATGCCTGTGTA 240

Qy 241 CCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAACATG 300

Qy 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Qy 361 CTAAAGCCCATGTGTAAATTAACCCCTCTGTGTTACTTTAAATTCACACTAATTTGAAT 420

Db 361 CTAAAGCCCATGTGTAAATTAACCCCTCTGTGTTACTTTAAATTCACACTAATTTGAAT 420

Qy 421 ATCATAAGAATACTACTAATCCCTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Db 421 ATCATAAGAATACTACTAATCCCTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Qy 481 ATAAAAAATTGCTCTTCTATATCACCACAAGCATAAAGAAATAAGGTAAGAAAGAAATAT 540

Db 481 ATAAAAAATTGCTCTTCTATATCACCACAAGCATAAAGAAATAAGGTAAGAAAGAAATAT 540

Qy 541 GCACCTTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAACTAAGTATAGG 600

Db 541 GCACCTTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAACTAAGTATAGG 600



Qy 601 TTAATAAGTTGTAAACACCTCAGTCATTACACAGGCGCTGTCCAAAGGTATCCTTTTCAGCCA 660  
Db |||||  
Qy 601 TTAATAAGTTGTAAACACCTCAGTCATTACACAGGCGCTGTCCAAAGGTATCCTTTTCAGCCA 660  
Db |||||  
Qy 661 ATTCCCATACATTATTGTGTCCGGCTGGGTTTGCATGCTAAAGTGTAACAATAAGACA 720  
Db |||||  
Qy 661 ATTCCCATACATTATTGTGTCCGGCTGGGTTTGCATGCTAAAGTGTAACAATAAGACA 720  
Db |||||  
Qy 721 TTCAATGGATCAGGACCATGCACAAATGTCCAGCACAGTACAATGTACACATGGAATTAGG 780  
Db |||||  
Qy 721 TTCAATGGATCAGGACCATGCACAAATGTCCAGCACAGTACAATGTACACATGGAATTAGG 780  
Db |||||  
Qy 781 CCAGTGGTGTCAACTCAACTGCTGTCTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840  
Db |||||  
Qy 781 CCAGTGGTGTCAACTCAACTGCTGTCTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840  
Db |||||  
Qy 841 AGATCTGAAAAATTTCCAGACACAATGCTAAACCATATAGTACAGCTAAATGAATCTGTA 900  
Db |||||  
Qy 841 AGATCTGAAAAATTTCCAGACACAATGCTAAACCATATAGTACAGCTAAATGAATCTGTA 900  
Db |||||  
Qy 901 GTAAATTAATTGTACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACCAAGG 960  
Db |||||  
Qy 901 GTAAATTAATTGTACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACCAAGG 960  
Db |||||  
Qy 961 AGAGCATTTTATGCAAGAAGAAACATAAATAGGAGATATAAGACAAGCACATTGTAAACATT 1020  
Db |||||  
Qy 1021 AGTAGACAAAAATGGAATAACACTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTT 1080  
Db |||||  
Qy 1021 AGTAGACAAAAATGGAATAACACTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTT 1080  
Db |||||  
Qy 1081 AGGAATAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCAC 1140  
Db |||||  
Qy 1081 AGGAATAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCAC 1140  
Db |||||  
Qy 1141 AGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCAAACTGTTTAAATAGTACT 1200  
Db |||||  
Qy 1141 AGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCAAACTGTTTAAATAGTACT 1200  
Db |||||  
Qy 1201 TGGAAATGTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAAATGC 1260  
Db |||||  
Qy 1201 TGGAAATGTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAAATGC 1260  
Db |||||  
Qy 1261 AGAATAAAACAAATTTATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320  
Db |||||  
Qy 1261 AGAATAAAACAAATTTATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320  
Db |||||  
Qy 1321 ATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGA 1380  
Db |||||  
Qy 1321 ATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGA 1380  
Db |||||  
Qy 1381 GGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGAC 1440  
Db |||||  
Qy 1381 GGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGAC 1440  
Db |||||  
Qy 1441 AATTGGAGAAGTGAATTATATAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA 1500  
Db |||||  
Qy 1441 AATTGGAGAAGTGAATTATATAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA 1500  
Db |||||  
Qy 1501 CCCACCAGGCAAAAGAGAAGAACAGTGCACAAAGAGAAAAAGAGGGGAGCGGTTTCAGGA 1560  
Db |||||  
Qy 1501 CCCACCAGGCAAAAGAGAAGAACAGTGCACAAAGAGAAAAA----- 1540  
Db |||||  
Qy 1561 GGTGGAGGTTCTGGAGGTGGCGGATCGGATCCAAAGAGGTTGGACAAAGATAGAAGATGAA 1620  
Db |||||  
Qy 1541 -----GACCGGATCCAAAGAGGTTGGACAAAGATAGAAGATGAA 1578  
Db |||||  
Qy 1621 AGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA 1680  
Db |||||  
Qy 1579 AGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA 1638  
Db |||||

Qy 1681 AGATCCTTATCCTTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAG 1740  
Db |||||  
Qy 1639 AGATCCTTATCCTTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAG 1698  
Db |||||  
Qy 1741 GATATAATGTTAAACAAGAGAGAGACGAAGAAAGAAAACAGACTTTGAAATGCAAAAAGGT 1800  
Db |||||  
Qy 1699 GATATAATGTTAAACAAGAGAGAGACGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGT 1758  
Db |||||  
Qy 1801 GATCAGAAATCCTCAAAATTGCGGCACATGTCTATAAGTGAGGCCAGCAGTAAACAACATCT 1860  
Db |||||  
Qy 1759 GATCAGAAATCCTCAAAATTGCGGCACATGTCTATAAGTGAGGCCAGCAGTAAACAACATCT 1818  
Db |||||  
Qy 1861 GTGTTACAGTGGGCTGAAAAAGGATACCTACACCATGAGCAACAACCTTGGTAACCCCTGGAA 1920  
Db |||||  
Qy 1819 GTGTTACAGTGGGCTGAAAAAGGATACCTACACCATGAGCAACAACCTTGGTAACCCCTGGAA 1878  
Db |||||  
Qy 1921 AATGGGAAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980  
Db |||||  
Qy 1879 AATGGGAAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1938  
Db |||||  
Qy 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATATAGCCAGCTCTGCCTAAAAG 2040  
Db |||||  
Qy 1939 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATATAGCCAGCTCTGCCTAAAAG 1998  
Db |||||  
Qy 2041 TCCCCCGGTAGATTTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAA 2100  
Db |||||  
Qy 1999 TCCCCCGGTAGATTTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAA 2058  
Db |||||  
Qy 2101 CTTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCCAGGTGCTTCG 2160  
Db |||||  
Qy 2059 CTTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCCAGGTGCTTCG 2118  
Db |||||  
Qy 2161 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTT 2220  
Db |||||  
Qy 2119 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTT 2178  
Db |||||  
Qy 2221 GGTTACTCAAACTCGAGTGATAATCTAGAT 2251  
Db |||||  
Qy 2179 GGTTACTCAAACTCGAGTGATAATCTAGAT 2209  
Db |||||

RESULT 3

AAF82930  
ID AAF82930 standard; cDNA; 2070 BP.

XX AAF82930;

XX 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)

XX HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.  
DE Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX Human immunodeficiency virus 1.

OS Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 13..2070

FT sig\_peptide /\*tag= a

FT /\*tag= b

FT misc\_feature /note= "synthetic secretory signal peptide"

FT 73..1542

FT /\*tag= c

FT /note= "HIV-1 gp120 domain coding sequence"

FT 1543..1593

FT /\*tag= d

FT /note= "[Gly4Ser]3 linker coding sequence"

FT 1594..2070

FT misc\_feature /\*tag= e

/note= "human CD154 short form extracellular domain coding sequence"

WO200126608-A2.

19-APR-2001.

13-OCT-2000; 2000WO-US028414.

14-OCT-1999; 99US-0159690P.

(LEDB/) LEDBETTER J A.  
(HAYD/) HAYDEN-LED BETTER M S.

Ledbetter JA, Hayden-Ledbetter MS;  
WPI; 2001-281790/29.  
P-PSDB; AAB62335.

DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

Example 1; Fig 3B; 55pp; English.

The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by (Gly4Ser)3 linker. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;

Query Match 83.5%; Score 1880; DB 4; Length 2070;  
Best Local Similarity 92.0%; Pred. No. 0;  
Matches 2070; Conservative 0; Mismatches 0; Indels 180; Gaps 1

QY 1 AAGCTTGCCGCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTTGGATCTCG 60  
Db |||||||  
QY 1 AAGCTTGCCGCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTTGGATCTCG 60  
Db |||||||  
QY 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAATTGTGG 120  
Db {}|||||  
QY 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAATTGTGG 120  
Db |||||||  
QY 121 GTCACAGTCTATTATGGGGTACCCTGTGTGGAGAGAAGCAACCACCTCTATTTGTGCA 180  
Db |||||||  
QY 121 GTCACAGTCTATTATGGGGTACCCTGTGTGGAGAGAAGCAACCACCTCTATTTGTGCA 180  
Db |||||||  
QY 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA 240  
Db |||||||  
QY 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA 240  
Db |||||||  
QY 241 CCCACAGACCCCACCCACAAGAACAGTAGTATTGGGAATGTGACAGAAAAATTTAACATG 300  
Db |||||||  
QY 241 CCCACAGACCCCACCCACAAGAACAGTAGTATTGGGAATGTGACAGAAAAATTTAACATG 300  
Db |||||||  
QY 301 TGGAAAAATAACATGGTAGATCATGTCATGAGGATATAATCAGTTTATGGGATGAAAGC 360  
Db |||||||  
QY 301 TGGAAAAATAACATGGTAGATCATGTCATGAGGATATAATCAGTTTATGGGATGAAAGC 360  
Db |||||||  
QY 361 CTAAAGCCATGTGTAAATAAACCACCTCTGTGTTACTTTAAATGCACATAATTGAAT 420  
Db |||||||  
QY 361 CTAAAGCCATGTGTAAATAAACCACCTCTGTGTTACTTTAAATGCACATAATTGAAT 420  
Db |||||||  
QY 421 ATC ACTA AGA ATA C TA AT CC CA C TA GT AC GA GG AA TG AT GG AG AA GG AG AA 480  
Db |||||||  
QY 421 ATC ACTA AGA ATA C TA AT CC CA C TA GT AC GA GG AA TG AT GG AG AA GG AG AA 480  
Db |||||||  
QY 481 ATAAAAAATTGCTCTTTCTATPATCACCAAGCATAAAGAAATAAGGTAAAGAAAGATAT 540  
Db |||||||

Db 1561 GGTGGAGGTTCTGGAGGTGGCGGATCGGATCC----- 1592

QY 1621 AGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA 1680

Db 1593 ----- 1592

QY 1681 AGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAG 1740

Db 1593 ----- 1592

QY 1741 GATATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGT 1800

Db 1593 -----AGAAAACAGCTTTGAAATGCAAAAAGGT 1620

QY 1801 GATCAGAATCCTCAAAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAAACAACATCT 1860

Db 1621 GATCAGAATCCTCAAAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAAACAACATCT 1680

QY 1861 GTGTTACAGTGGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCCCTGGAA 1920

Db 1681 GTGTTACAGTGGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCCCTGGAA 1740

QY 1921 AATGGGAAACAGCTGACCGTTTAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACC 1980

Db 1741 AATGGGAAACAGCTGACCGTTTAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACC 1800

QY 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAG 2040

Db 1801 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAG 1860

QY 2041 TCCCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 2100

Db 1861 TCCCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 1920

QY 2101 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCG 2160

Db 1921 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCG 1980

QY 2161 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCCTTT 2220

Db 1981 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCCTTT 2040

QY 2221 GGCTTACTCAAACCTCGAGTGATAATCTAGA 2250

Db 2041 GGCTTACTCAAACCTCGAGTGATAATCTAGA 2070

RESULT 4  
AAF82931

ID AAF82931 standard; cDNA; 2028 BP.

XX AC AAF82931;

XX DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.

XX KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX FH Key Location/Qualifiers

CDS 13..2028

FT /\*tag= a

FT sig\_peptide 13..72

FT /\*tag= b

FT /\*note= "synthetic secretory signal peptide"

FT 73..1542

FT misc\_feature /\*tag= c

FT misc\_feature /note= "HIV-1 gp120 domain coding sequence"

FT 1543..1551

FT /\*tag= d

FT /note= "ProAspPro linker coding sequence"

FT 1552..2028

FT /\*tag= e

FT /note= "human CD154 short form extracellular domain coding sequence"

XX WO200126608-A2.

PN 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028414.

XX 14-OCT-1999; 99US-0159690P.

PR (LEDB/) LEDBETTER J A.

XX (HAYD/) HAYDEN-LEDBETTER M S.

PA Ledbetter JA, Hayden-Ledbetter MS;

PI

XX WPI; 2001-281790/29.

DR P-PSDB; AAB62336.

DR

XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PT

PT

XX

PS Example 1; Fig 3B; 55pp; English.

XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be use against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)

CC

XX

SQ Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;

Query Match 79.3%; Score 1786.4; DB 4; Length 2028;

Best Local Similarity 89.9%; Pred. No. 0;

Matches 2022; Conservative 0; Mismatches 6; Indels 222; Gaps 1;

QY 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Db 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

QY 61 GCTTCGAGATCTATGCTCCITGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCCATGCTCCITGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

QY 121 GTCACAGTCTATTATGGGGTACCTGTGGAGAGAAGCAACCACTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGGTACCTGTGGAGAGAAGCAACCACTCTATTTTGTGCA 180

QY 181 TCAGATGCTAAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA 240

Db 181 TCAGATGCTAAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA 240

QY 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

QY 301 TGGAAAAATAAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

QY 361 CTAAGCCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATAATTGAAT 420

Db 361 CTAAGCCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATAATTGAAT 420



Qy	421	ATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA	480
Dd	421		
Qy	481	ATAAAAAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAGGTAAAGAAAGAAATAT	540
Dd	481		
Qy	541	GCACTTTTTAATAGACTTGATGTAGTACCAATAGAAAATACTAATAATACTAAGTATAGG	600
Dd	541		
Qy	601	TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCTTTCAGCCA	660
Dd	601		
Qy	661	ATTCATACATTATTGTGTCCCGCTGGGTTTGGCATGCTAAAGTGTAACAATAAGACA	720
Dd	661		
Qy	721	TTCAATGGATCAGGACCATGCACAAATGTACGACACAGTACAAATGTACACATGGAATTAGG	780
Dd	721		
Qy	781	CCAGTGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT	840
Dd	781		
Qy	841	AGATCTGAAAAATTTACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA	900
Dd	841		
Qy	901	GTAATTAATTGTACAAGACCCAAACAATACAAGAAGAGGTTATCTATAGGACCAAGG	960
Dd	901		
Qy	961	AGAGCAATTTATGCAAGAAGAAACATAATAGGAGATATAAGCAAGCACATTGTAAACATT	1020
Dd	961		
Qy	1021	AGTAGACAAAATGGAATAACACTTTACAAACAGATAGTTATAAAAATTAAGAGAAAAATTT	1080
Dd	1021		
Qy	1081	AGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCAC	1140
Dd	1081		
Qy	1141	AGTTTAAATTGTGAGGGGAAATCTTCTACTGTAATACAGCAAACTGTTTAATAGTACT	1200
Dd	1141		
Qy	1201	TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC	1260
Dd	1201		
Qy	1261	AGAAATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCC	1320
Dd	1261		
Qy	1321	ATCAGAGCAAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGA	1380
Dd	1321		
Qy	1381	GGTAATAGTACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGAC	1440
Dd	1381		
Qy	1441	AATTGGAGAAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA	1500
Dd	1441		

Qy	1501	CCCAACAGGGCAAAGAGAAAGACAGTGCAAAAGAGAAAAAGAGGGGAGCGGTTTCAGGA	1560
Dd	1501		
Qy	1561	GGTGGAGGTTCTGGAGGTTGGCGGATCGGATCCAAGAAAGGTTGGACAAGATAGAAGATGAA	1620
Dd	1547	-----	1546
Qy	1621	AGGAATCTTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA	1680
Dd	1547	-----	1546
Qy	1681	AGATCCTTATCCTTACTGAACCTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAG	1740
Dd	1547	-----	1546
Qy	1741	GATATAATGTTAAACAAAGAGGAGACGAAAGAAAGAAAAACAGACTTTGAAATGCAAAAAAGGT	1800
Dd	1547	-----	1578
Qy	1801	GATCAGAATCCTCAAAATTTGCGGCACATGTCTATAAGTGAGCCAGCAGTAAACAAACATCT	1860
Dd	1579	GATCAGAATCCTCAAAATTTGCGGCACATGTCTATAAGTGAGCCAGCAGTAAACAAACATCT	1638
Qy	1861	GTGTTACAGTGGGCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTTGAA	1920
Dd	1639	GTGTTACAGTGGGCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTTGAA	1698
Qy	1921	AATGGGAAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC	1980
Dd	1699	AATGGGAAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC	1758
Qy	1981	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATAGCCAGCCTCTGCTTAAAG	2040
Dd	1759	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATAGCCAGCCTCTGCTTAAAG	1818
Qy	2041	TCCCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA	2100
Dd	1819	TCCCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA	1878
Qy	2101	CCTTGGGGGCAACAATCCAATTCACCTTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCG	2160
Dd	1879	CCTTGGGGGCAACAATCCAATTCACCTTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCG	1938
Qy	2161	GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAAGTCCCTTT	2220
Dd	1939	GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAAGTCCCTTT	1998
Qy	2221	GGCTTACTCAAACTCGAGTGATAATCTAGA	2250
Dd	1999	GGCTTACTCAAACTCGAGTGATAATCTAGA	2028

RESULT 5  
ACA63265  
ID ACA63265 standard; DNA; 2046 BP.  
XX  
AC ACA63265;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE HIV-1 immunogenic sequence #1.  
XX  
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
immunogenic; virucide; ds.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO2004001051-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 20-JUN-2003; 2003WO-EP007146.

```
XX PR 20-JUN-2002; 2002EP-00291550.
XX PA (INSP ) INST PASTEUR.
XX PA (CNRS ) CENT NAT RECH SCI.
XX
XX Tangy F, Lorin C, Mollet L, Delebecque F;
XX WPI; 2004-082508/08.
XX
XX New recombinant mononegavirales measles virus expressing a heterologous
XX PT amino acid, useful for preparing immunogenic or vaccine composition for
XX PT the prophylaxis or treatment of measles.
XX
XX Disclosure; Fig 16A; Opp; English.
XX
XX The present invention relates to a recombinant mononegavirales measles
XX CC virus expressing a heterologous amino acid, which is capable of eliciting
XX CC a humoral and/or cellular immune response against the heterologous amino
XX CC acid sequence including in individuals having pre-existing measles virus
XX CC immunity. The recombinant virus is useful for preparing immunogenic or
XX CC vaccine composition for the prophylaxis or treatment of measles. The
XX CC present sequence is a HIV immunogenic sequence shown in the
XX CC exemplification of the invention
XX
XX Sequence 2046 BP; 741 A; 328 C; 475 G; 502 T; 0 U; 0 Other;
XX
XX Query Match 64.5%; Score 1452.6; DB 12; Length 2046;
XX Best Local Similarity 98.1%; Pred. No. 5.5e-296;
XX Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
XX
XX 52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 37 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 96
XX
XX 112 AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 97 AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 156
XX
XX 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
XX
XX 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAT 291
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAT 276
XX
XX 292 TTTTAACATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATATCAGTTTATGG 351
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 277 TTTTAACATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATATCAGTTTATGG 336
XX
XX 352 GATGAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACT 411
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 337 GATGAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACT 396
XX
XX 412 AATTGAATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG 471
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 397 AATTGAATATCACTAAGAATACTACTAATCTCACTAGTAGCAGCTGGGGAATGATGGAG 456
XX
XX 472 AAAGGAGAAATAAAAAATTGCTCTTCTATATCACCACAGCATAAAGAAATAAGGTAAG 531
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 457 GAAGGAGAAATAAAAAATTGCTCTTCTATATCACCACAGCATAAAGAAATAAGGTAAG 516
XX
XX 532 AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT 591
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 517 AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAGTAAAAATACTAGTAATACT 576
XX
XX 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAGGTATCC 651
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAGGTATCC 636
XX
XX 652 TTTTCAGCCAATTCCCATACATTATTGTCCCGGCTGGGTTTGGCATGCTAAAGTGTAAC 711
XX ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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```
Db 637 TTTTCAGCCAAATCCCATACATTATTGTGTCCCGGCTGGGTTTGGGATACTAAAGTGTAAAC 696
QY 712 AATAAGACATTCAATGGATCAGGACCATGCACAATGTGCAGCACAGTACAATGTACACAT 771
Db 697 AATAAGACATTCAATGGATCAGGACCATGCACAATGTGCAGCACAGTACAATGTACACAT 756
QY 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGAC 831
Db 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGAC 816
QY 832 ATAGTAATTAGATCTGAAAAATTTTCACAGACAAATGCTAAAAACCATAATAGTACAGCTAAAT 891
Db 817 ATAGTAATTAGATCTGAAGATTTTCACAGACAAATGTTAAAAACCATAATAGTACAGCTAAAT 876
QY 892 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATA 951
Db 877 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATA 936
QY 952 GGACCAGGGAGAGCAATTTTATGCAAGAAGAAACAATAATAGGAGATATAAGACAAGCACAT 1011
Db 937 GGACCAGGGAGAGCAATTTTATGCAAGAAGAAACAATAATAGGAGATATAAGACAAGCACAT 996
QY 1012 TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGA 1071
Db 997 TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGA 1056
QY 1072 GAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCCAGAAATT 1131
Db 1057 GAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCCAGAAATT 1116
QY 1132 GTAATGCACAGTTTTTAATTGTGGAGGGGAATTCCTTACTGTAAATACAGCACAACTGTTT 1191
Db 1117 GTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAAATACAGCACAACTGTTT 1176
QY 1192 AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1251
Db 1177 AATAGTACTTGGAAATGTTCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1236
QY 1252 CTCCAATGCAGAATAAAACAAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1311
Db 1237 CTCCAATGCAGAATAAAACAAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1296
QY 1312 GCCCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAAACA 1371
Db 1297 GCCCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAAACA 1356
QY 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431
Db 1357 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1416
QY 1432 ATGAGGGACAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1491
Db 1417 ATGAGGGACAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1476
QY 1492 GGAGTAGCACCCACCAGGGCAAGAGAAACACAGTGCAAAAGAGAAAAAGAGGGGGAGG 1550
Db 1477 GGAGTAGCACCCACCAGGGCAAGAGAAACACAGTGCAAAAGAGAAAAAGAGCAGTGGG 1535
RESULT 6
ACA63266
ID ACA63266 standard; DNA; 2610 BP.
XX ACA63266;
AC ACA63266;
XX
DT 22-APR-2004 (first entry)
XX
DE HIV-1 immunogenic sequence #2.
XX
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;
KW immunogenic; virucide; ds.
XX
OS Human immunodeficiency virus type 1.
```





DE HIV truncated envelope glycoprotein 160 coding sequence.

XX HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;

KW gene; ds; anti-HIV; truncated.

KW Human immunodeficiency virus.

OS

XX Key Location/Qualifiers

FH 1..2001

FT /\*tag= a

FT /product= "truncated gp 160"

XX

PN WO2003077838-A2.

XX

PD 25-SEP-2003.

XX

XX 05-MAR-2002; 2002WO-US007144.

PF

XX 05-MAR-2002; 2002WO-US007144.

PR (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.

XX

PA

XX Dimitrov DS, Chow Y, Phogat SK, Broder CC;

PI

XX WPI; 2003-779074/73.

DR P-PSDB; ABU64219.

DR

XX New HIV antigenic composition comprising an HIV envelope glycoprotein 160

PT having a glycoprotein 120 subunit covalently linked to a glycoprotein 41

PT subunit useful for protecting a human from HIV infection.

PT

XX Disclosure; Page 62-63; 65pp; English.

PS

XX The present invention relates to an HIV antigenic composition, comprising

CC an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41

CC subunit, where the carboxy-terminal end of gp120 is covalently linked

CC through a peptide linker of at least 5 amino acids, to the amino-terminal

CC end of gp41. The HIV antigenic composition is useful for protecting a

CC human from HIV infection, potentially in the form of a vaccine. The

CC present sequence is the HIV truncated gp160 coding sequence

XX

SQ Sequence 2051 BP; 749 A; 333 C; 467 G; 502 T; 0 U; 0 Other;

Query Match 64.3%; Score 1448; DB 10; Length 2051;

Best Local Similarity 99.1%; Pred. No. 5.1e-295;

Matches 1467; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 74 TGCTCCTGGGATATTGATGATCTGTAGTGCT--ACAGAAAAATTGTGGGTACAGTCT 130

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

53 TGCTCCTGGGATGTTGATGATCTGTAGTGCTGCAAAAGAAAAACGTGGTCACAATCT 112

QY 131 ATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTA 190

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

113 ATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTA 172

QY 191 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACC 250

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

173 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACC 232

QY 251 CCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGGAAAAATA 310

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

233 CCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGGAAAAATA 292

QY 311 ACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCAT 370

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

293 ACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCAT 352

QY 371 GTGTAAATTAACCCCACTCTGTGTACTTTAAATTGCACATAATTGAATATCACTAAGA 430

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

353 GTGTAAATTAACCCCACTCTGTGTACTTTAAATTGCACATAATTGAATATCACTAAGA 412

QY 431 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAAAATT 490

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 413 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAAAATT 472

QY 491 GCTCTTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGTAAAGAAAGAAATATGCACITTTTA 550

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

473 GCTCTTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGTAAAGAAAGAAATATGCACITTTTA 532

QY 551 ATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTTAATAAGTT 610

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

533 ATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTTAATAAGTT 592

QY 611 GTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAATTTCCCATAC 670

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

593 GTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAATTTCCCATAC 652

QY 671 ATTATTGTGTCCCGCTGGGTTTGCATGCTAAAGTCTAAACAATAAGACATTCATTAAGTAT 730

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

653 ATTATTGTGTCCCGCTGGGTTTGCATGCTAAAGTCTAAACAATAAGACATTCATTAAGTAT 712

QY 731 CAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGTGT 790

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

713 CAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGTGT 772

QY 791 CAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAACATAGTAATTAGATCTGAAA 850

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

773 CAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAACATAGTAATTAGATCTGAAA 832

QY 851 ATTTACAGACAATGCTTAAACCATAATAAGTACAGCTTAAATGAATCTGTAGTAATTAATT 910

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

833 ATTTACAGACAATGCTTAAACCATAATAAGTACAGCTTAAATGAATCTGTAGTAATTAATT 892

QY 911 GTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCATTTT 970

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

893 GTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCATTTT 952

QY 971 ATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTTAGTAGACAA 1030

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

953 ATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTTAGTAGACAA 1012

QY 1031 AATGGAATAACACITTTTACAACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAATAAAA 1090

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1013 AATGGAATAACACITTTTACAACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAATAAAA 1072

QY 1091 CAATAGCCTTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCACAGTTTTAATT 1150

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1073 CAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCACAGTTTTAATT 1132

QY 1151 GTGAGGGGAATTCCTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTTGGAATGTTA 1210

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1133 GTGAGGGGAATTTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTTGGAATGTTA 1192

QY 1211 CTGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAAAAC 1270

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1193 CTGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAAAAC 1252

QY 1271 AAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGGAC 1330

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1253 AAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGGAC 1312

QY 1331 AAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAGAGATGGAGGTAATAGTA 1390

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1313 AAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAGAGATGGAGGTAATAGTA 1372

QY 1391 CTGAGACTGAGACTGAGATCTTCAGACCTGGAGGGAGAGATATGAGGGACAATTTGGAGAA 1450

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1373 CTGAGACTGAGACTGAGATCTTCAGACCTGGAGGGAGAGATATGAGGGACAATTTGGAGAA 1432

QY 1451 GTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAGGG 1510

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1433 GTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAGGG 1492

QY 1511 CAAAGAGAAAGAACAGTGCAAAAGAGAAAAAGAGGGGGAGG 1550

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

1493 CAAAGAGAAAGAACAGTGCAAAAGAGAAAAAGAGCAGTGGG 1532











|||||  
Db 1141 AATAGTACTTGGAAATGTTGCTGGAGGACAAATGGCACTGAAGGAAATGACATAATCACA 1200  
QY 1252 CTCCAATGCAGAATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAGCAATGTAT 1311  
Db 1201 CTCCAATGCAGAATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAGCAATGTAT 1260  
QY 1312 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTAACA 1371  
Db 1261 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTAACA 1320  
QY 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431  
Db 1321 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1380  
QY 1432 ATGAGGGACAAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1491  
Db 1381 ATGAGGGACAAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1440  
QY 1492 GGAGTAGCACCCACCAGGGCAAGAGAAAGAACAGTGCAAGAGAAAAAGAGGGGGAGG 1550  
Db 1441 GGAGTAGCACCCACCAGGGCAAGAGAAAGAACAGTGCAAGAGAAAAAGAGCGAGTGGG 1499

RESULT 11  
AAX04767  
ID AAX04767 standard; DNA; 3806 BP.  
XX  
AC AAX04767;  
XX  
DT 17-OCT-2003 (revised)  
DT 09-APR-1999 (first entry)  
XX  
DE Env gene of the BA-L strain of Human immunodeficiency virus type 1.  
XX  
KW HIV-1; HIV-1 strain BA-L; env protein; vaccine; immunotherapy;  
KW HIV infection; immunogen; HIV-1 diagnosis; ds.  
XX  
OS Human immunodeficiency virus 1.

XX  
FH Location/Qualifiers  
FT CDS 648..3214  
FT /\*tag= a  
FT /product= "env\_protein"  
FT /transl\_except= (pos: 678..678, aa: Gln)

XX  
PN US5869313-A.  
XX  
XX  
PD 09-FEB-1999.  
XX  
XX  
PF 14-MAY-1996; 96US-00647714.  
XX  
XX  
PR 17-OCT-1990; 90US-00599491.  
PR 25-FEB-1993; 93US-00022835.  
PR 15-FEB-1995; 95US-00388809.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX  
XX Gallo RC, Franchini G, Reitz MS, Lori FC, Popovic M, Gartner S;  
PI Markham PD;  
PI  
XX  
DR WPI; 1999-152779/13.  
DR P-PSDB; AAW88113.  
DR

XX  
PT DNA encoding env protein of the human immune deficiency virus isolate BA-  
PT L - useful for producing protein for use in vaccines, as assay reagent  
PT and to generate antibodies.  
XX  
XX Claim 2; Fig 8A-H; 87pp; English.  
PS  
XX  
XX The present sequence encodes the envelope protein of the BA-L (ATCC  
CC 40890) strain of Human immunodeficiency virus type 1 (HIV-1) strain MN-  
CC ST1. BA-L is more typical of United States isolates of HIV-1 than

CC previously known strains. Recombinant, complete env protein of the BA-L  
CC strain is used as a vaccine component and for immunotherapy of existing  
CC HIV infections, to detect HIV-specific antibodies, e.g. in donated blood,  
CC and as an immunogen to raise specific antibodies, for HIV-1 diagnosis.  
CC (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 3806 BP; 1306 A; 662 C; 937 G; 901 T; 0 U; 0 Other;  
  
Query Match 54.4%; Score 1225.2; DB 2; Length 3806;  
Best Local Similarity 90.1%; Pred. No. 4.7e-248;  
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;  
  
QY 73 ATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTGTGGGTCACAGTCTAT 132  
Db 701 ATGCTCCTTGGGATATTAAATGATCTGTAATGCTGAAGAAAAATTGTGGGTCACAGTCTAT 760  
QY 133 TATGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGCTAAA 192  
Db 761 FATGGGTACCTGTGTGGAAGAAGCAACCACCTCTATTTTGTGCATCAGATCGTAAA 820  
QY 193 GCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 252  
Db 821 GCATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 880  
QY 253 AACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGAAAAAATAAC 312  
Db 881 AACCCACAAGAGTAGAATTGAAAAATGTGACAGAAAAATTTAAACATGTGAAAAAATAAC 940  
QY 313 ATGGTAGATCAGATGCATCAGGATATAATCAGTTTATGSGATGAAAGCCTAAAGCCATGT 372  
Db 941 ATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCCTAAAGCCATGT 1000  
QY 373 GTAAAAATTAAACCCACTCTGTGTTACTTTTAAATTGCACTAATTGA-----ATATCACT 426  
Db 1001 GTAAAAATTAAACCCACTCTGTGTTACTTTTAAATTGCACTGATTGAGGAATGCTACTAAT 1060  
QY 427 AAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAA 486  
Db 1061 GGGAAATGACACTAATACCCTAGTAGTAGCAGGGGAATGTTGGGGGAGGAGAAATGAAA 1120  
QY 487 AATTGCTCTTTCTATATCACCAACAGCATAAAGAAATAAGSTPAAAGAAAAAATATGCATT 546  
Db 1121 AATTGCTCTTTCAATATACCAACAAACATAAAGAGGTAGGTGCAGAAAAAGATATGCATT 1180  
QY 547 TTTAATAGACTTGTATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAATA 606  
Db 1181 TTTTATAAACCCTTGATATAGCACCATAAGATAATAATAGTAATAATAGATATAGGTTGATA 1240  
QY 607 AGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATCCC 666  
Db 1241 AGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTGAGCCCAATCCC 1300  
QY 667 ATACATTATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACATTCAAT 726  
Db 1301 ATACATTATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAAGATAAGAAGTTCAAT 1360  
QY 727 GGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTG 786  
Db 1361 GGAAGAGGACCATGTACAAATGTCTAGCACAGTACAATGTACACATGGAATTAGGCCAGTA 1420  
QY 787 GTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCT 846  
Db 1421 GTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGGTAGTAATTAGATCC 1480  
QY 847 GAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT 906  
Db 1481 GCCAATTCGCGGACAATGCTAAAAGTCATAAATAGTACAGCTGAATGAATCTGTAGAAAT 1540  
QY 907 AATTGTACAAGACCCCAACAATAACAAGAAAGGTTATCTATAGGACCAGGGAGAGCA 966  
Db 1541 AATTGTACAAGACCCCAACAATAACAAGAAAGTATACATATAGGACCAGGCAGAGCA 1600  
QY 967 TTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGTA 1026

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Dbb 1601 TTTTATACACAGGAGAAATAATAGGAGATATAAGACAAGCACATGTGAACCTTAGTAGA 1660
Qy 1027 GCAAAATGGAATAACACTTTTACACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAAT 1086
Db 1661 GCAAAATGGAATGACACTTTTAAATAGATAGTTATATAAAATTAAGAGAAACAATTTGGGAAT 1720
Qy 1087 AAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTAATGCACAGTTTT 1146
Db 1721 AAAACAATAGCTTTAAGCACTCCTCAGGAGGGGACCCAGAAATTTGTGACGCACAGTTTT 1780
Qy 1147 AATTGTGAGGGGAATTCTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTGGAAAT 1206
Db 1781 AATTGTGAGGGGAATTTTCTACTGTAATTCACACAACACTGTTTAATAGTACTTGGAAAT 1840
Qy 1207 GTTACTGAGGGACAAATGGCACCTGAAGGAATGACATAATCACACTCCAATGCAGATA 1266
Db 1841 GTTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACACAATCACACTCCCATGCAGATA 1900
Qy 1267 AAACAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACA 1326
Db 1901 AAACAATTAATAACATGTGGCAGGAAGTAGGAAGAGCAATGTATGCCCTCCCATCAGA 1960
Qy 1327 GGACAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAGAGATGGAGTAAT 1386
Db 1961 GGACAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG---T 2017
Qy 1387 AGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGG 1446
Db 2018 CCTGAGGACAAACAAGCCGAGGCTTCAGACCTGGAGGAGGAGATATGAGGGATAATTGG 2077
Qy 1447 AGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCACC 1506
Db 2078 AGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCACC 2137
Qy 1507 AGGCAAGAGAGAAACAGTGCAAGAGAAAAAGAGGGGGAGG 1550
Db 2138 AAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAAGAGCAGTGCG 2181
```

RESULT 12  
AAT58551  
ID AAT58551 standard; cDNA; 3807 BP.

```

XX AC AAT58551;
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX Human Immunodeficiency Virus-1 strain BA-L env gene.
DE Acquired immune deficiency syndrome; AIDS; envelope protein; env gene;
KW vaccine; ds.
XX Human immunodeficiency virus 1; (strain BA-L).
XX Key Location/Qualifiers
FT CDS 648..3215
FT /*tag= a
FT /product= "envelope_protein"
XX US5576000-A.
XX 19-NOV-1996.
XX 15-FEB-1995; 95US-00388809.
XX 17-OCT-1990; 90US-00599491.
PR 25-FEB-1993; 93US-00022835.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
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PI Gallo RC, Franchini G, Lori FC, Popovic M, Reitz MS, Gartner S;
PI Markham PD;
XX WPI; 1997-011206/01.
DR P-PSDB; AAW11581.
XX New isolated envelope protein of HIV-1 strain BA-L and recombinant
PT equivalents - useful as immunogens for vaccines and antibody prodn.,
PT typical of US clinical isolates.
XX Example; Fig 8; 86pp; English.
PS A HindIII fragment of unintegrated viral DNA representing the BA-L genome
CC was cloned into lambda phage Charon 28 DNA from total DNA of peripheral
CC blood lymphocytes infected with and producing HIV-1(BA-L). A positive
CC clone was selected by hybridisation using a HIV-1 env probe. This clone,
CC designated BA-L1, was found to contain the entire gene for the envelope
CC protein on a 2.8 kb HindIII-XbaI fragment and a 0.4 kb EcoRI-HindIII
CC fragment. When cloned together these fragments comprise the env gene, as
CC well as the coding regions for rev and the rev-responsive element of env,
CC both necessary for efficient expression in eukaryotic cells. The claimed
CC recombinantly produced envelope protein can be used as an immunogen for
CC raising antibodies against HIV. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3807 BP; 1307 A; 662 C; 937 G; 901 T; 0 U; 0 Other;

Query Match 54.4%; Score 1225.2; DB 2; Length 3807;
Best Local Similarity 90.1%; Pred. No. 4.7e-248;
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

Qy 73 ATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGGGTCACAGTCTAT 132
Db 702 ATGCTCCTTGGGATATTGATGATCTGTAAATGCTGAAGAAAAATTTGGGTCACAGTCTAT 761

Qy 133 TATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGCTAAA 192
Db 762 TATGGGGTACCTGTGTGGAAAAAGCAACCACCTCTATTTTGTGCATCAGATGCTAAA 821

Qy 193 GCCTATGATACAGAGGTACATAAATGTTGGGCCACACATGCCTGTGTACCCACAGACCCC 252
Db 822 GCATATGATACAGAGGTACATAAATGTTGGGCCACACATGCCTGTGTACCCACAGACCCC 881

Qy 253 AACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAATAAAC 312
Db 882 AACCCACAAGAGTAGAATTGAAAAATGTGACAGAAAAATTTTAAACATGTGGAATAAAC 941

Qy 313 ATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATGT 372
Db 942 ATGCTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCCTAAAGCCATGT 1001

Qy 373 GTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCACATAATTGA-----ATATCACT 426
Db 1002 GTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCACATAATTGAGGAATGCTACTAAT 1061

Qy 427 AAGAATACTACTAATCCCCTAGTAGCAGCTGGGGAATGATGGAGAAAAGGAGAAATAAAA 486
Db 1062 GCGAATGACACTAATACCACTAGTAGTAGCAGGGGAATGTTGGGGGAGGAGAAATGAAA 1121

Qy 487 AATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACCT 546
Db 1122 AATTGCTCTTTCAATATACCAACACATAAGAGGTAGGTGCAGAAAGAAATATGCACCT 1181

Qy 547 TTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAATA 606
Db 1182 TTTTATAAAGCTTGATATAGCAACCAATAGATAATAATAGTAATAATAGATATAGGTTGATA 1241

Qy 607 AGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTTCAGCCAATCCC 666
Db 1242 AGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTTCAGCCAATCCC 1301

Qy 667 ATACATTATTGTGTCGCCGGCTGGGTTTTCGATGCTAAAGTGAACAATAAGACATTCAAT 726
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Db 1302 ATACATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAAAGATAAGAAAGTTCAAT 1361

Qy 727 GGATCAGGACCATGCACAAATGTTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTG 786

Db 1362 GGAAGAGGCATGTACAAATGTTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTA 1421

Qy 787 GTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATCT 846

Db 1422 GTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCC 1481

Qy 847 GAAATTTTCACAGACAAATGCTAAACCAATAATAGTACGCTAAATGAATCTGTAGTAATT 906

Db 1482 GCCAATTTGCGGACAATGCTAAAGTCATAANTAGTACAGCTGAATGAATCTGTAGAAAT 1541

Qy 907 AATTGTACAAGACCCCAACAATAACAAGAAGGTTTATCTATATAGGACCAGGGAGAGCA 966

Db 1542 AATTGTACAAGACCCCAACAATAACAAGAAAAGTATACATATAGGACCAGGCAGAGCA 1601

Qy 967 TTTTATGCAAGAAGAAACATAATAGGAGATATAAGACACAGCACATTGTAACATTAGTAGA 1026

Db 1602 TTTTATACAACAGGAGAAATAATAGGAGATATAAGACACAGCACATTGTAACCTTAGTAGA 1661

Qy 1027 GCAAAATGGAATAACACCTTTCAACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAAT 1086

Db 1662 GCAAAATGGAATGACACCTTTAAATAAGATAGTTATAAAATTAAGAGAACAAATTTGGGAAT 1721

Qy 1087 AAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAATGCACAGTTTT 1146

Db 1722 AAAACAATAGTCTTTAAGCACTCCTCAGGAGGGACCCAGAAAATTGTGACGCACAGTTTT 1781

Qy 1147 AATTGTGAGGGGAATTTCTTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAAAT 1206

Db 1782 AATTGTGAGGGGAATTTTCTTACTGTAAATTCACACAACTGTTTAAATAGTACTTTGGAAAT 1841

Qy 1207 GTTACTGAGGGACAAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAATA 1266

Db 1842 GTTACTGAAGAGTCAAATAACACTGTAGAAAATAACACAATCACACTCCCATGCAGAATA 1901

Qy 1267 AAACAAATTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACA 1326

Db 1902 AAACAAATTATAACATGTGGCAGGAAGTAGGAAGAGCAATGTATGCCCTCCCATCAGA 1961

Qy 1327 GGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTTAACAAGAGATGGAGGTAAT 1386

Db 1962 GGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG---T 2018

Qy 1387 AGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGG 1446

Db 2019 CCTGAGGACAAACAAGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGATAATTGG 2078

Qy 1447 AGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAAACCATAGGAGTAGCACCCACC 1506

Db 2079 AGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAAACCATTAGGAGTAGCACCCACC 2138

Qy 1507 AGGGCAAAGAGAAAGACAGTGCAAGAGAGAAAAAGAGGGGAGG 1550

Db 2139 AAGGCAAAGAGAGAGTGGTGCAGAGAGAAAAAGAGCAGTGGG 2182

RESULT 13

ADO52562

ID ADO52562 standard; DNA; 9540 BP.

XX

AC ADO52562;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human immunodeficiency virus 1 parent JRCSF DNA.

XX

KW Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy;

KW vaccine; ds.

XX

OS Human immunodeficiency virus 1.

XX US2004101823-A1.

PN

XX 27-MAY-2004.

PD

XX 19-DEC-2002; 2002US-00325468.

PF

XX 21-DEC-2001; 2001US-0343524P.

PR

XX (MAXY-) MAXYGEN INC.

PA

XX Soong NW, Pekrun K, Shibata R;

PI

XX WPI; 2004-399670/37.

XX GENBANK; M38429.

DR

DR New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a composition for treating or preventing infection caused by HIV-1.

XX

PS Disclosure; SEQ ID NO 46; 310pp; English.

XX

CC The present invention relates to human immunodeficiency virus 1 (HIV-1) viral variants and nucleic acids and polypeptides thereof having improved replication properties for development of suitable animal models for the study of HIV-1 pathogenesis. The invention is useful for treating and preventing HIV-1 infection. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the invention.

XX

SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 54.3%; Score 1222.2; DB 12; Length 9540;

Best Local Similarity 90.3%; Pred. No. 2.4e-247;

Matches 1334; Conservative 0; Mismatches 128; Indels 15; Gaps 2;

Qy 74 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGGGTACAGTCTATT 133

Db 6291 TGCTCCTTGGGACATTAAATGATCTGTAGTGTCTAGAAAAAGTTGTGGGTACAGTCTATT 6350

Qy 134 ATGGGTACCTGTGTGGAGAGAGCAACACCACCTCTATTTTGTGCATCAGATGCTAAAG 193

Db 6351 ATGGGTACCTGTGTGGAAGAGAAACAACCACCTCTATTTTGTGCATCAGATGCTAAAG 6410

Qy 194 CCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCCACAGACCCCA 253

Db 6411 CATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCCACAGACCCCA 6470

Qy 254 ACCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAATAACA 313

Db 6471 ACCACAAGAAGTAGTATTGGGAAATGTAAACAGAAGATTTTAAACATGTGGAAAAATAACA 6530

Qy 314 TGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATGTG 373

Db 6531 TGGTAGAACAGATGCAGGAGGATGTAATCAATTTATGGGATCAAAGCTTAAAGCCATGTG 6590

Qy 374 TAAAAATTAACCCCACTCTGTGTACTTTTAAATTGCACATAATTGAATATCACTAAGAATA 433

Db 6591 TAAAAATTAACCCCACTCTGTGTACTTTTAAATTGCAAAGATGT-----GAATG 6638

Qy 434 CTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAGAAAAATAAAAAATTGCT 493

Db 6639 CTACTAATACCACTAGTAGTAGTGAGGGAATGATGGAGAGAGGAGAGAAAAATAAAAACTGCT 6698

Qy 494 CTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGAAAGATATGCACTTTTTAATA 553

Db 6699 CTTTCAATATCACCAAAAGCATAAAGATAGAGATAAGGTGCAGAAAGAAATATGCTCTTTTATA 6758

Qy 554 GACTTGATGTAGTACCAATAGAAAATACTAATAATACTAAGTATAGGTTAATAAGTTGTA 613

Db 6759 AACTGGATGTAGTACCAATAGATAATAAGAAATAATACCAATAATAGGTTAATAAGTTGTA 6818

Qy 614 ACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTTCAGCCAATTTCCCATACATT 673



||||| 6819 ACACCTCAGTCATTACACAAGCCCTGTCCAAAGGTATCCTTTGAACCAATTCCTCATACATT 6878

Qy 674 ATTGTGTCCGGCTGGTTTGGCATGTGTAAGTGTAAACAATAAGACATTCAATGGATCAG 733

Db 6879 ATTGTGCCCGCTGGTTTTCGCAATCTTAAAGTGTAAATAAAGACATTCAATGGAAAAG 6938

Qy 734 GACCATGCACAAATGTCCAGCACAGTACAAATGTACACATGGAATTAGCCAGTGGTGCA 793

Db 6939 GACAATGTAAAAATGTCCAGCACAGTACAAATGTACACATGGAATTAGCCAGTAGTATCAA 6998

Qy 794 CTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATCTGAAAATT 853

Db 6999 CTCAACTGCTGCTAAATGGCAGTCTAGCAGAAGAAGGTTGTAATTAGATCTGCACAATT 7058

Qy 854 TCACAGACAATGCTAAACCATAATAGTACAGCTAAATGAATCTGTAGTAATTAATTGTA 913

Db 7059 TTACGGACAATGCTAAACCATAATAGTACAGCTGAATGAATCTGTAAAAATTAATTGTA 7118

Qy 914 CAAGACCCCAACAATAACAGAGAAGGTTATCTATAGGACAGGGAGAGCATTTTATG 973

Db 7119 CAAGGCCAGCAACAATAACAGAAAAAGTATACATATAGGACAGGGAGAGCATTTTATA 7178

Qy 974 CAAGAAGAAACATAATAGGAGATATAAGACAAAGCACATTGTAACATTAGTAGAGCAAAAT 1033

Db 7179 CAACAGGAGAAATAATAGGAGATATAAGACAAAGCACATTGTAACATTAGTAGAGCACAAT 7238

Qy 1034 GGAATAACACTTTACAACAGATAGTTATAAAATTAAAGAGAAAAATTTAGGAATAAAACAA 1093

Db 7239 GGAATAACACTTTAAACACAGATAGTTGAAAAATTAAAGAGAACAAATTTAATAATAAAACAA 7298

Qy 1094 TAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAATTGTAATGCACAGTTTTTAATTGTG 1153

Db 7299 TAGTCTTTACTCACTCCTCAGGAGGGGATCCAGAAATTGTAATGCACAGTTTTTAATTGTG 7358

Qy 1154 GAGGGAATTTCTTCTACTGTATACAGCACAACTGTTTAAATAGTACTTTGGAATGTTACTG 1213

Db 7359 GAGGGAATTTTCTACTGTAAATCAACACAACTGTTTAAATAGTACTTTGGAATGATACTG 7418

Qy 1214 GAGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAGAAATAAAACAA 1273

Db 7419 AAAAGTCAAGTGGCACTGAAGGAATGACACCATCATACTCCCATGCAGAAATAAAACAA 7478

Qy 1274 TTATAAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGGACAA 1333

Db 7479 TTATAAACATGTGGCAGGAAGTGGGAAAGCAATGTATGCTCTCCCATTAAGGACAA 7538

Qy 1334 TTAGATGTTCAATAATATTACAGGCTGCTACTAACAAGAGATGGAGGTAATAGTACTG 1393

Db 7539 TTAGATGTTCAATAATATTACAGGCTGCTATTAAACAAGAGATGGTGGTAA---AAATG 7595

Qy 1394 AGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAGTG 1453

Db 7596 AGAGTGAGATCGAGATCTTCAGACCTGGAGGAGGAGACATGAGGGACAATTTGGAGAGTG 7655

Qy 1454 AATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCGGCA 1513

Db 7656 AATTATATAAATATAAAGTAGTAAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCA 7715

Qy 1514 AGAGAAGAACAGTGCAAGAGAAAAAGAGGGGAGG 1550

Db 7716 AGAGAAGAGTGGTGCAAGAGAAAAAGAGCAGTGGG 7752

RESULT 14

ADP20074

ID ADP20074 standard; DNA; 9540 BP.

XX AC ADP20074;

XX DT 09-SEP-2004 (first entry)

XX DE Human immunodeficiency virus 1 isolate JRCSF nucleotide sequence.

XX immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;

KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;

KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSF;

KW gene; ds.

XX Human immunodeficiency virus 1.

OS

XX

PH Location/Qualifiers

FT LTR 1..635

FT /\*tag= a

FT /partial

FT 790..2304

FT /\*tag= b

FT /product= "gag"

FT 2085..5108

FT /\*tag= c

FT /product= "pol"

FT 5053..5631

FT /\*tag= d

FT /product= "vif"

FT 5571..5861

FT /\*tag= e

FT /product= "vpr"

FT 6073..6318

FT /\*tag= f

FT /product= "vpU"

FT 6236..8782

FT /\*tag= g

FT /product= "env"

FT 8784..9434

FT /\*tag= h

FT /product= "nef"

FT 9103..9540

FT /\*tag= i

FT /partial

XX WO2004053100-A2.

XX 24-JUN-2004.

XX 11-DEC-2003; 2003WO-US039534.

XX 11-DEC-2002; 2002US-0432869P.

XX 24-APR-2003; 2003US-0465350P.

XX (SCRI ) SCRIPPS RES INST.

XX Burton DR, Wilson I, Pantophlet R;

XX WPI; 2004-480933/45.

XX P-PSDB; ADP20067, ADP20068, ADP20069, ADP20070, ADP20071, ADP20072,

XX ADP20073.

XX GENBANK; M38429.

XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against

PT the polypeptide, useful preventing or treating human immunodeficiency

PT virus (HIV) infection, especially HIV-1 infection.

XX Disclosure; Page 139-141; 149pp; English.

PS

XX

CC The present invention describes an immunogenic mutant HIV gp120

CC polypeptide that can stimulate a neutralising antibody response against a

CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic

CC mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising

CC antibody response against a panel of HIV-1 comprising HIV-1 primary

CC isolates of at least two different clades, where the mutant gp120 has at

CC least one amino acid mutation in at least one epitope of the HIV-1 gp120

CC polypeptide specifically bound by a neutralising antibody, which reduces

CC binding affinity of the non-neutralising antibody; (2) an immunogenic

CC mutant HIV-1 gp120 polypeptide (Ib) having at least one amino acid

CC mutation in at least one epitope of the gp120 polypeptide specifically

CC bound by a non-neutralising antibody; (3) a vaccine (II) comprising one

CC or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5)  
CC an isolated HIV neutralising antibody (IV) fraction obtained by using  
CC (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V)  
CC obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in  
CC a subject, by administering an HIV neutralising antibody produced in  
CC response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV  
CC -1 infection in a human subject, involves administering HIV-1  
CC neutralising antibodies to the subject, where the HIV-1 neutralising  
CC antibodies comprise antibodies stimulated in response to (II); (9) HIV  
CC neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV  
CC neutralising antibodies (VII) obtained by using (Ib); and (II) isolated  
CC HIV-1 neutralising antibodies obtained by harvesting spleen and lymph  
CC nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV  
CC activities, and can be used in vaccines and in HIV binding agents. (Ia)  
CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1  
CC which involves immunising a subject with a (Ia) or (Ib). The antibodies  
CC are useful for preventing or ameliorating HIV, especially HIV-1,  
CC infection in a subject. The present sequence represents an HIV-1 isolate  
CC JRCSEF genomic nucleotide sequence, which is given in the exemplification  
CC of the present invention.  
XX

SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 54.3%; Score 1222.2; DB 12; Length 9540;  
Best Local Similarity 90.3%; Pred. No. 2.4e-247;  
Matches 1334; Conservative 0; Mismatches 128; Indels 15; Gaps 2;

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DB 7059 TTACGGACAATGCTAAAAACCATAATAGTACAGCTGAATGAATCTGTAAAAATTAATTGTA 7118  
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DB 7716 AGAGAAGAGTGGTGCAAGAGAGAAAAAGAGCAGTGGG 7752

RESULT 15  
AAQ14753

ID AAQ14753 standard; DNA; 3807 BP.

XX AAQ14753;

XX AC AAQ14753;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 17-DEC-2001 (revised)

XX DT 05-FEB-1992 (first entry)

XX DE HIV-1 BA-L clone.

XX human immunodeficiency virus; United States; MN isolate; AIDS;

XX KW envelope protein; ss.

XX OS Human immunodeficiency virus 1.

PH	Key	Location/Qualifiers
FT	CDS	394..476
FT		/*tag= b
FT		/product= "rev"
FT	CDS	648..3215
FT		/*tag= a
FT		/product= "env"
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PN	USN7599491-N.	
XX		
PD	15-OCT-1991.	
XX		
PF	17-OCT-1990;	90US-00183830.
XX		
PR	17-OCT-1990;	90US-00599491.
XX		
PA	(USSH ) NAT INST OF HEALTH.	
XX		
PI	Reitz M;	
XX		
DR	WPI; 1991-346752/47.	
DR	P-PSDB; AAR14905.	
XX		
PT	US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in	
PT	therapeutics, vaccines and diagnostic tests.	
XX		
PS	Example 3; Fig 8; 61pp; English.	
XX		
CC	A HindIII fragment of unintegrated viral DNA representing the HIV-1 (BA-	
CC	L) genome was cloned by standard techniques into lambda phage Charon 28	
CC	DNA from total DNA of peripheral blood macrophages infected with and	
CC	producing HIV-1 (BA-L). A positive clone was selected by hybridisation	
CC	using a HIV-1 envelope probe. This clone, designated BA-L1, contained the	
CC	entire env gene. The insert was subcloned and sequenced. The BA-L plasmid	
CC	clone has been deposited as ATCC 40890. The sequence also contains the	
CC	coding region for the rev protein which is needed for efficient	
CC	expression of the envelope protein in eukaryotic cells. (Note: Revised	
CC	entry submitted to correct the patent number format of US Government-	
CC	owned NTIS applications to prevent clashes with ongoing US granted patent	
CC	numbers. For further information please visit the Derwent web site at	
CC	www.derwent.com/dwpi/updates/ntis us.html.) (Updated on 25-MAR-2003 to	
CC	correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)	
XX		
SQ	Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;	
	Query Match 54.1%; Score 1218.8; DB 2; Length 3807;	
	Best Local Similarity 89.8%; Pred. No. 1e-246;	
	Matches 1333; Conservative 0; Mismatches 142; Indels 9; Gaps 2;	
Qy	73 ATGCTCCTGGGATATTGATGATCTGTAGTGCTACAGAAAATTGTGGGTACAGTCTAT 132	
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	702 ATGCTCCTGGGATATTGATGATCTGTAATGCTGAAGAAAATTGTGGGTACAGTCTAT 761	
Qy	133 TATGGGTACCTGTGTGGAGAGAGCAACCACCCTCTATTTTGTGCATCAGATGCTAAA 192	
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	1062 GGGAAATGACACTAATACCACTAGTAGTAGCAGGGGAATGGTGGGGGAGGAGAAATGAAA 1121	
Qy	487 AATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACTT 546	
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	1122 AATTGCTCTTTCAATATCACCAAAACATAAGAGGTAAAGGTGAGAAAGAAATATGCACCT 1181	
Qy	547 TTTAATAGACTTGTAGTAGTACCAATAGAAAATATCTAAATACTAATAGTATAGGTTAATA 606	
Db		
	1182 TTTATAAACTTTGATATAGCACCAATAGATAATAATAGTAATAATAGTATAGGTTGATA 1241	
Qy	607 AGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTTCAGCCAATTTCCC 666	
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	2019 CCTGAGGACAACAAGACCCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGATTAATTTGG 2078	
Qy	1447 AGAAGTGAATTATATATAATAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCCACC 1506	
Db		
	2079 AGAAGTGAATTATATAATAATAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCCACC 2138	
Qy	1507 AGGGCAAAGAGAGAAACAGTGCAAAAGAGAAAAAAGAGGGGAGG 1550	

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Search completed: November 12, 2004, 01:29:25  
Job time : 751.71 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 131.432 Seconds  
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1225.2	54.4	3807	1 US-08-388-809-5	Sequence 5, Appli
3	1225.2	54.4	3807	2 US-08-647-714-5	Sequence 5, Appli
4	1173.4	52.1	4527	2 US-08-944-449-8	Sequence 8, Appli
5	1173.4	52.1	4527	3 US-09-353-362-8	Sequence 8, Appli
6	1172.6	52.1	3807	2 US-08-417-210A-78	Sequence 78, Appl
7	1172.6	52.1	3807	4 US-09-136-159A-78	Sequence 78, Appl
8	1172.4	52.1	2571	1 US-08-254-358-3	Sequence 3, Appli
9	1172.4	52.1	2571	1 US-08-475-391-3	Sequence 3, Appli
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13	1172.4	52.1	2571	5 PCT-US95-07178-3	Sequence 3, Appli
14	1172.4	52.1	6474	3 US-08-651-472-66	Sequence 66, Appl
15	1172.4	52.1	6474	3 US-08-358-928-66	Sequence 66, Appl
16	1172.4	52.1	6926	3 US-08-651-472-69	Sequence 69, Appl
17	1172.4	52.1	6926	3 US-08-358-928-69	Sequence 69, Appl
18	1172.4	52.1	9739	1 US-08-022-835-1	Sequence 1, Appli
19	1172.4	52.1	9739	1 US-08-388-809-1	Sequence 1, Appli
20	1172.4	52.1	9739	2 US-08-647-714-1	Sequence 1, Appli
21	1172.4	52.1	9746	1 US-08-022-835-3	Sequence 3, Appli
22	1172.4	52.1	9746	1 US-08-388-809-3	Sequence 3, Appli
23	1172.4	52.1	9746	2 US-08-647-714-3	Sequence 3, Appli
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26	1171.8	52.0	2552	3 US-09-492-739-27	Sequence 27, Appl
27	1171.4	52.0	1539	3 US-07-956-483-21	Sequence 21, Appl

28	1171.4	52.0	1539	3 US-08-472-240A-13	Sequence 13, Appl
29	1168.6	51.9	1532	2 US-08-037-816A-15	Sequence 15, Appl
30	1168.6	51.9	1532	2 US-08-530-146-15	Sequence 15, Appl
31	1168.6	51.9	2573	2 US-08-448-603A-29	Sequence 29, Appl
32	1168.6	51.9	2573	3 US-09-134-075-29	Sequence 29, Appl
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34	1165.4	51.7	1532	2 US-08-037-816A-27	Sequence 27, Appl
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37	1162.2	51.6	9737	3 US-09-353-362-7	Sequence 7, Appli
38	1162	51.6	1932	4 US-09-475-515-31	Sequence 31, Appl
39	1162	51.6	2457	4 US-09-475-515-32	Sequence 32, Appl
40	1161	51.6	1419	4 US-09-475-515-30	Sequence 30, Appl
41	1160.8	51.5	1929	4 US-09-602-864-12	Sequence 12, Appl
42	1160.4	51.5	2570	2 US-08-448-603A-31	Sequence 31, Appl
43	1160.4	51.5	2570	3 US-09-134-075-31	Sequence 31, Appl
44	1160.4	51.5	2570	3 US-09-492-739-31	Sequence 31, Appl
45	1158.4	51.4	1527	3 US-07-956-483-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-08-022-835-5  
; Sequence 5, Application US/08022835  
; Patent No. 5420030  
; GENERAL INFORMATION:  
; APPLICANT: Reitz Jr., Marvin S.  
; APPLICANT: Franchini, Genoveffa  
; APPLICANT: Markham, Phillip D.  
; APPLICANT: Gallo, Robert C.  
; APPLICANT: Lori, Franco C.  
; APPLICANT: Popovic, Mikulas  
; APPLICANT: Garnter, Suzanne  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/022,835  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scott, Watson T.  
; REGISTRATION NUMBER: 26,581  
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3807 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS

LOCATION: 648..3215  
US-08-022-835-5  
Query Match 54.4%; Score 1225.2; DB 1; Length 3807;  
Best Local Similarity 90.1%; Pred. No. 1.4e-293;  
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;  
QY 73 ATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGGTCCACAGTCTAT 132  
DB 702 ATGCTCCTTGGGATATTAAATGATCTGTAATGCTGAAGAAAAATTGTGGTCCACAGTCTAT 761  
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DB 762 TATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATCGTAAA 821  
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QY 313 ATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAAAGCCTAAAGCCATGT 372  
DB 942 ATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGATCAAAGCCTAAAGCCATGT 1001  
QY 373 GTAAAAATTAACCCCACTCTGTGTACTTTAAATTTGCCTAAATTTGA-----ATATCACT 426  
DB 1002 GTAAAAATTAACCCCACTCTGTGTACTTTAAATTTGCCTGATTTGAGGAATGCTACTAAT 1061  
QY 427 AAGATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAFAAAA 486  
DB 1062 GGGATGACACTAATACCACCTAGTAGTAGCAGGGGAATGTGGGGGAGGAGAAATGAAA 1121  
QY 487 AATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAGAAAGAAATATGCACCT 546  
DB 1122 AATTGCTCTTTCAATATCACCACAACATAAGAGGTAAAGTGCAGAAAGAAATATGCACCT 1181  
QY 547 TTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAAATAACTAAGTATAGTTAATA 606  
DB 1182 TTTATAAACTTGATATAGCAACCAATAGATAATAATAGTAATAATAGATATAGTTGATA 1241  
QY 607 AGTTGTAAACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTAGGCCAAATCCC 666  
DB 1242 AGTTGTAAACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTAGGCCAAATCCC 1301  
QY 667 ATACATTATTGTGTCCCGCTGGGTTTGCATGTCTAAAGTGTAAACAATAAGACATTCAAT 726  
DB 1302 ATACATTATTGTGCCCCGGCTGTTTTCGATTCTAAAGTGTAAAGATAAGAGTTCAAT 1361  
QY 727 GGATCAGGACCATGACAAATGTGAGCACAGTACAAATGTACACATGGAATTAGGCCAGTG 786  
DB 1362 GGAAAGGACCATGTACAAATGTGAGCACAGTACAAATGTACACATGGAATTAGGCCAGTA 1421  
QY 787 GTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTAGATCT 846  
DB 1422 GTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAGGTAGTAATTAGATCC 1481  
QY 847 GAAAATTTACAGACAATGCTTAAACCATAATAGTACAGCTAAATGAATCTGTAGTAATT 906  
DB 1482 GCCAATTTGCGGACAATGCTTAAATGCTATAATAGTACAGCTGAATGAATCTGTAGAAAT 1541  
QY 907 AATTGTACAAGACCCCAACAATFACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCA 966  
DB 1542 AATTGTACAAGACCCCAACAATFACAAGAAAAAGTATACATATAGGACCAGGCAGAGCA 1601  
QY 967 TTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTAGA 1026  
DB 1602 TTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTTGTAACCTTAGTAGA 1661  
QY 1027 GCAAAATGGAATAACACTTTACACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAAT 1086

DB 1662 GCAAAATGGAATGACACTTTAAATAAGATAGTTATAAAATTAAGAGAAACAATTTGGGAAT 1721  
QY 1087 AAAACAATAGCCTTTAATCAATCTCTCAGGAGGGAGCCAGAAAATTTGTAATGCACAGTTTT 1146  
DB 1722 AAAACAATAGTCTTTAAGCACTCTCTCAGGAGGGAGCCAGAAAATTTGTACGCACAGTTTT 1781  
QY 1147 AATTGTGAGGGGAATTTCTTCTACTGTAAATACAGCACAACACTGTTTAAATAGTACTTTGGAAT 1206  
DB 1782 AATTGTGAGGGGAATTTTCTACTGTAAATCAACACAACACTGTTTAAATAGTACTTTGGAAT 1841  
QY 1207 GTTACTGGAGGGACAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAATA 1266  
DB 1842 GTTACTGAAGAGTCAATAAACACTGTAGAAAAATAACAATCACACTCCCATGCAGAATA 1901  
QY 1267 AAACAAATTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACA 1326  
DB 1902 AAACAAATTATAACATGTGGCAGGAAGTAGGAAGAGCAATGTATGCCCTCCCATCAGA 1961  
QY 1327 GGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGTAAT 1386  
DB 1962 GGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--T 2018  
QY 1387 AGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAAFTGG 1446  
DB 2019 CCTGAGGACAACAAGACCGAGGTCTTCAGACCTGGAGGAGAGATATGAGGGATAATGG 2078  
QY 1447 AGAAGTGAATTATATAATAATAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCACC 1506  
DB 2079 AGAAGTGAATTATATAATAATAAGTAGTAAAAATTTGAACCATTAGGAGTAGCACCACC 2138  
QY 1507 AGGGCAAAGAGAAGACAGTGCAAAAGAGAAAAAAGAGGGGGAGG 1550  
DB 2139 AAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGG 2182

RESULT 2

US-08-388-809-5  
; Sequence 5, Application US/08388809  
; Patent No. 5576000  
; GENERAL INFORMATION:  
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT  
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
; APPLICANT: GARTNER, SUZANNE  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK, 3.5"  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,809  
; FILING DATE: 15-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,835  
; FILING DATE: 25-FEB-1993  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LESLIE A. SERUNIAN  
; REGISTRATION NUMBER: 35,353  
; REFERENCE/DOCKET NUMBER: 2026-4092US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800





```

; APPLICATION NUMBER: US/08/388,809
; FILING DATE: 15-FEB-1995
; APPLICATION NUMBER: US 08/022,835
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: LESLIE A. SERUNIAN
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4092US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3215
US-08-647-714-5

Query Match          54.4%; Score 1225.2; DB 2; Length 3807;
Best Local Similarity 90.1%; Pred. No. 1.4e-293;
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 73 ATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAAATTGTGGGTCACAGTCTAT 132
   |||||
Db 702 ATGCTCCTTGGGATATTAAATGATCTGTAATGCTGAAGAAAAAATTGTGGGTCACAGTCTAT 761

QY 133 TATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATGCTAAA 192
   |||||
Db 762 TATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATCGTAAA 821

QY 193 GCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCC 252
   |||||
Db 822 GCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCC 881

QY 253 AACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAAC 312
   |||||
Db 882 AACCCACAAGAAAGTAGAATTGAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAAC 941

QY 313 ATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAAGCCATGT 372
   |||||
Db 942 ATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGT 1001

QY 373 GTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCACATAATTGA-----ATATCACT 426
   |||||
Db 1002 GTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCACATGATTGAGGAATGCTACTAAT 1061

QY 427 AAGAACTACTATAATCCCACTAGTACGAGCTGGGGAATGATGGAGAAAGGAGAAAAATAAA 486
   |||||
Db 1062 GGGAAATGACACTAATACCACTAGTAGCAGGGGAATGTTGGGGGAGGAGAAATGAAA 1121

QY 487 AATTGCTCTTTCTATATCACCACAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACCTT 546
   |||||
Db 1122 AATTGCTCTTTCAATATCACCACAAACATAAGAGGTAAAGGTGAGGTGAGAAAAAGAAATATGCACCTT 1181

QY 547 TTTTAATAGACTTGATGTAGTACCRAATAGAAAAATACTAATAATACTAAGTATAGGTTAATA 606
   |||||
Db 1182 TTTTATAAACTTGATATAGCACCAATAGATAATAATAGTAAATAATAGATATAGGTTGATA 1241

QY 607 AGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTCAGCCCAATCCC 666
   |||||
Db 1242 AGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTCAGCCCAATCCC 1301

QY 667 ATACATTATTGTGTCCTCCGGCTGGGTTTGGCATGCTAAAGTGTAAACAATAAGACATTCAAT 726
   |||||
Db 1302 ATACATTATTGTGCCCCGGCTGGGTTTGGGATCTTAAAGTGTAAAGATAAGAAAGTTCAAT 1361
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QY 727 GGATCAGGACCATGCACAAAATGTGAGCAGTACAGTACAAATGTACACATGGAATTAGCCAGTG 786
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Db 1362 GGAAAAGGACCATGTACAAAATGTGAGCAGTACAGTACAAATGTACACATGGAATTAGCCAGTA 1421

QY 787 GTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCT 846
   |||
Db 1422 GTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGGAGGTAGTAATTAGATCC 1481

QY 847 GAAAATTTTCACAGACAATGCTAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT 906
   |||
Db 1482 GCCAATTTTCGGGACAATGCTAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1541

QY 907 AATTGTACAAGACCCCAACAACAATACAAGAAAGAGGTTATCTATAGGACCAGGGAGAGCA 966
   |||
Db 1542 AATTGTACAAGACCCCAACAACAATACAAGAAAAAGTATACATATAGGACCAGGCAGAGCA 1601

QY 967 TTTTATGCAAGAAAGAACATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGTAGA 1026
   |||
Db 1602 TTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAAACCTTAGTAGA 1661

QY 1027 GCAAAAATGGAATAACACTTTACAACAGATAGTTATPAAAAATTAAGAGAAAAATTTAGGAAT 1086
   |||
Db 1662 GCAAAAATGGAATGACACTTTAAATAAGATAGTTATAAAAATTAAGAGAACAAATTTGGGAAT 1721

QY 1087 AAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCACAGAAAATTTGTAATGCACAGTTT 1146
   |||
Db 1722 AAAACAATAGTCTTTAAGCACTCCTCAGGAGGGGGCCAGAAAATTTGTACGCACAGTTT 1781

QY 1147 AATTGTGGAGGGGAATTTCTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAAT 1206
   |||
Db 1782 AATTGTGGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAAATAGTACTTTGGAAT 1841

QY 1207 GTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAATA 1266
   |||
Db 1842 GTTACTGAAGAGTCAAATAACACTGTAGAAAATAACAATCACACTCCCATGCAGAATA 1901

QY 1267 AAACAAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACA 1326
   |||
Db 1902 AAACAAAATTATAAACAATGTGGCAGGAAAGTAGGAAAGCAATGTATGCCCTCCCATCAGA 1961

QY 1327 GGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAAT 1386
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Db 1962 GGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGTGG---T 2018

QY 1387 AGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTTGG 1446
   |||
Db 2019 CCTGAGGACAACAAGACCCGAGTCTTCAGACCTGGAGGAGGAGATATGAGGGATAATTGG 2078

QY 1447 AGAAGTGAATTATATAATAATAAGTAGTAAGAATTGAAACCAATAGGAGTAGCACCACC 1506
   |||
Db 2079 AGAAGTGAATTATATAATAATAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCACC 2138

QY 1507 AGGCAAAAGAGAAGAACACAGTCCAAAGAGAAAAAAGAGGGGGAGG 1550
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Db 2139 AAGCAAAAGAGAAGAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGG 2182

RESULT 4
US-08-944-449-8
; Sequence 8, Application US/08944449
; Patent No. 5985613
; GENERAL INFORMATION:
; APPLICANT: KURTH, REINHARD
; APPLICANT: BAIER, MICHAEL
; APPLICANT: MEYNER, KARIN
; APPLICANT: WERNER, ALBRECHT
; TITLE OF INVENTION: Use of an "immunodeficiency-virus suppressing
; TITLE OF INVENTION: lymphokine (iSL)" to inhibit the replication of
; TITLE OF INVENTION: viruses, particularly of retroviruses
; FILE REFERENCE: 8341-7065
; CURRENT APPLICATION NUMBER: US/08/944,449
; CURRENT FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: EP 95113013.2
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; EARLIER FILING DATE: 1995-08-18  
; EARLIER APPLICATION NUMBER: DE 195 13 152.5  
; EARLIER FILING DATE: 1995-04-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8

; LENGTH: 4527  
; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1  
US-08-944-449-8

Query Match 52.1%; Score 1173.4; DB 2; Length 4527;  
Best Local Similarity 86.0%; Pred. No. 1e-280;  
Matches 1339; Conservative 0; Mismatches 206; Indels 12; Gaps 3;

Qy	52	TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	515	TGCTTGTGGAGATGGGCGACGATGCTCCTTGGGATGTTAATGATCTGTAGTGTGCAGAA	574
Qy	112	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTA	171
Db	575	AAATTGTGGGTACAGTCTTATTATGGGGTACCTGTGTGGAAAGATGCAACCCACTACTCTA	634
Qy	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	635	TTTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT	694
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAT	291
Db	695	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAT	754
Qy	292	TTTAAACATGTGGAAATAAATACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
Db	755	TTTAAACATGTGGAAATAAATACATGGTAGACCAGATGCATGAGGATATAGTCAGTTTATGG	814
Qy	352	GATGAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	411
Db	815	GATCAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	874
Qy	412	AAATTGAATATCACTAAGAATACCTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAG	471
Db	875	GATT-----ATTGGGAATGCTACTAATACCAACAATAGTAGTGGGGAACGGTGCAG	928
Qy	472	AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAG	531
Db	929	AAAGAAGAAATAAAAACTGCTCTTCAATATCACCACAAGCATAAAGGTAAGGTAAG	988
Qy	532	AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCATA--GAAATACTAATAAT	588
Db	989	AAGGCATATGCATATTTTAAATAACTTGATGTAGTACCATAAGATGATGATATACTAAT	1048
Qy	589	ACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCAATACAGGCCTGTCCAAAGGTA	648
Db	1049	ACCAGTATAGGTTGATACATTTGTAATTCCTCAGTCAATACAGACCTGTCCAAAGGTA	1108
Qy	649	TCCTTTCAGCCCAATCCCATACATATTGTGTCCCGGCTGGGTTTGCATGCTAAAGTGT	708
Db	1109	TCCTTTGAGCCCAATCCCTATACATATTGTGTCCCGGCTGGGTTTGCATGCTAAAGTGT	1168
Qy	709	AACAATAAGACATTTCAATGGATCAGGACCATGCACAAATGTGACAGTCAATGTACA	768
Db	1169	AATAATAAGAAGTTCAGTGGAAAAGGTCAATGTACAAATGTGACAGTCAATGTACA	1228
Qy	769	CATGGAATTAGGCCAGTGGTGTCAACTCAACTGTCTGTTTAAATGGCAGTCTAGCAGAGAA	828
Db	1229	CATGGAATTAGGCCAGTGGTGTCAACTCAACTGTCTGTTTAAATGGCAGTCTAGCAGAGAA	1288
Qy	829	GACATAGTAATTAGATCTGAAATTTTCAAGACAATGTGTAACCAATAGTACAGCTA	888
Db	1289	GAGTAGTAATTAGATCTGACAATTTTCAAGACAATGTGTAACCAATAGTACAGCTG	1348
Qy	889	AATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATAACAAGAAGGTTATCT	948

Db	1349	AATGTATCTGTAGAAATTAATTGTACAAGACCCCAACAATAAGAGAAGGATAACT	1408
Qy	949	ATAGGACCAGGAGAGCATTTTATGCAAGAAGAAAACATAATAGGAGATATAAGACAAGCA	1008
Db	1409	AGTGGACCAGGAAAGTACTTTATACAACAGGAGAAATAATAGGAGATATAAGAAAAGCA	1468
Qy	1009	CATTGTAAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTA	1068
Db	1469	TATTGTAAACATTAGTAGAGCAAAATGGAATAAAACCTTTAGAACAGGTAGCTACAAAATTA	1528
Qy	1069	AGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGACCCAGAA	1128
Db	1529	AGAGAAACAATTTGGGAATAAAACAATAGTATTTTAAACAATCCTCAGGAGGAGACCCAGAA	1588
Qy	1129	ATTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTGTAAACAGCAACAATCG	1188
Db	1589	ATTGTAATGCACAGTTTAAATTTGTAGAGGGGAATTTTCTACTGTAAACAACAACAATCG	1648
Qy	1189	TTTAATAGTACTTGGAAATGTTACTTGGAGGGACAAAATGSCACTGAAAGGAATGACATAATC	1248
Db	1649	TTTAATAGTACTTGGAAATGAAATAGTACTTGGAAATGCTACT--GGAAATGACACTATC	1705
Qy	1249	ACACTCCAATGCAGAAATAAAACAATAATTAATAATATGTGCAGAAAAGTAGGAAAAGCAATG	1308
Db	1706	ACACTCCCATGTAGAATAAAACAATAATTAACAATGTGCAGGAAGTAGGAAAAGCAATG	1765
Qy	1309	TATGCCCTCCCATCAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTA	1368
Db	1766	TATGCCCTCCCATCGAAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTA	1825
Qy	1369	ACAAGAGATGGAGTAAATAGTACTGAGACTGAGACTGAGACTCTTTCAGACCTGGAGGAGGA	1428
Db	1826	ACAAGAGATGGTGGTGGTGACAAGAACAGTACCACCGAGATCTTTAGACCTGCAGGAGGA	1885
Qy	1429	GATATGAGGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCA	1488
Db	1886	AATATGAAGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCA	1945
Qy	1489	ATAGGAGTAGCACCCACAGGGCAAGAGAAAGAACAGTGCAAAAGAGAAAAAGAGGGGGA	1548
Db	1946	TTAGGAGTAGCACCCACCAAGGCAAGAGAGAGAGTGGTGCAAAAGAGAAAAAGAGCAGTG	2005
Qy	1549	GGCGGTTTCAGGAGGTGGAGTTCTGGAGGTGGCGGATCGGATCCAAAGAGGTTGGAC	1605
Db	2006	GGAGTGATAGGAGCTATGTTCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGC	2062

RESULT 5

US-09-353-362-8

; Sequence 8, Application US/09353362

; Patent No. 6383739

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Use of an "immunodeficiency-virus suppressing

; TITLE OF INVENTION: lymphokine (ISL)" to inhibit the replication of viruses,

; TITLE OF INVENTION: in particular of retroviruses

; NUMBER OF SEQUENCES: 8

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/353,362

; FILING DATE: 15-JUL-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 195 13 152.5

; FILING DATE: 07-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95113013.2

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:



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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-417-210A-78

Query Match      52.1%; Score 1172.6; DB 2; Length 3807;
Best Local Similarity 88.1%; Pred. No. 1.5e-280;
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGTATGATGATCTGTAGTGCTACAGAA 111
Db 1668 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 1609

Qy 112 AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171
Db 1608 AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 1549

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 1548 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489

Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGTAAATGTGACAGAAAT 1429

Qy 292 TTTAATCATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
Db 1428 TTTAATCATGTGGAAAAATAACATGGTAGAAACAGATGCATGAGGATATAATCAGTTTATGG 1369

Qy 352 GATGAAAGCCTAAAGCCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATGCACT 411
Db 1368 GATCAAAGCCTAAAGCCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATGCACT 1309

Qy 412 AATTG-----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGG 459
Db 1308 GATTTGAGGAATACTACTAATACCAATAATAGTAGTCTGTATAAACAATAGTAATAGCGAG 1249

Qy 460 GGAATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATACCAACAAGCATAAGA 519
Db 1248 GGAACAATAAAGGGAGGAGAAATGAAAAAATGCTCTTTTCAATATACCAACAAGCATAAGA 1189

Qy 520 AATAAGGTAAGAAAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCAATAGAAAT 579
Db 1188 GATAAGATGCAGAAAGAAATATGCACTTCTTTATAAACTTGATATAGTATCAAT---AAAT 1132

Qy 580 ACTAATAATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGT 639
Db 1131 AATGATAGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT 1072

Qy 640 CCAAAGGTATCCTTTTCAGCCCAATTCACATACATTATTGTGTCGGGTGGGTTTGGCATG 699
Db 1071 CCAAAGATATCCTTTTGAGCCAATTCACATACATTATTGTGCCCGGCTGGTTTGGCATT 1012

Qy 700 CTAAAGTGTAAACAATAAGACATTTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTA 759
Db 1011 CTAAAGTGTAAACGATAAAAGTTTCAGTGGAAAGGATCATGTAAAAATGTCAGCACAGTA 952

Qy 760 CAATGTACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTA 819
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Db 951 CAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA 892
Qy 820 GCAGAAGAAGACATAGTAATTAGATCTGAAAATTTTCACAGACAATGCTAAAAACCATAATA 879
Db 891 GCAGAAGAAGAGGTAGTAATTAGATCTGAGAATTTCAATGATAAATGCTAAAAACCATCATA 832
Qy 880 GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGA 939
Db 831 GTACATCTGAATGAATCTGTACAAAATTAATTGTACAAGACCCCAACTACAATAAAGAAAA 772
Qy 940 AGGTTATCTATAGGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATA 999
Db 771 AGGATACATATAGGACCAGGGAGAGCATTTTATACAACAAAAAATATAATAGGAACATA 712
Qy 1000 AGACAAGCACATTTGTAACATTAGTAGAGCAAAAATGGAATTAACACTTTTACAACAGATAGTT 1059
Db 711 AGACAAGCACATTTGTAACATTAGTAGAGCAAAAATGGAATGACACTTTTAAGACAGATAGTT 652
Qy 1060 ATAAAAATTAAAGAGAAAAAATTTAGGAATAAAAAACAATAGCCTTTTAATCAATCCTCAGGAGG 1119
Db 651 AGCAAAATTAAAAGAACAAATTTAAGAATAAAAAACAATAGTCTTTAATCAATCCTCAGGAGG 592
Qy 1120 GACCAGAAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACA 1179
Db 591 GACCAGAAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATTCA 532
Qy 1180 GCACAACCTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGGACAAATGGCAGTGAAGG--A 1236
Db 531 TCACCACTGTTTAAATAGTACTTGGAAATGTTAAATACTTGGAAATAATACTACAGGGTCA 472
Qy 1237 AATGACATAAATCACACTCCAATGCAGAAATAAAACAAATTATAAATATGTGGCAGAAAGTA 1296
Db 471 AATAACAATAATCACACTTCAATGCAAAAATAAAACAAATTATAAACATGTGGCAGGAAGTA 412
Qy 1297 GGAAGAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACA 1356
Db 411 GGAAGAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA 352
Qy 1357 GGGCTGCTACTAACAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTC 1413
Db 351 GGGCTACTATTAAACAAGAGATGGTGGTAAGGACACGGACACGAAACGACACCGAGATCTTC 292
Qy 1414 AGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATATATAAATATAAAGTA 1473
Db 291 AGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATATATAAATATAAAGTA 232
Qy 1474 GTAAGAATTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAAAGAACAGTGCAAGA 1533
Db 231 GTAAACAATTGAACCATTAGGAGTAGCACCCACCACCAAGGCAAGAGAAAGAGTGGTGCAGAGA 172
Qy 1534 GAAAAAAGA 1542
Db 171 GAAAAAAGA 163
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RESULT 7  
US-09-136-159A-78/c  
; Sequence 78, Application US/09136159A  
; Patent No. 6596279  
; GENERAL INFORMATION:  
; APPLICANT: Virogenetics Corporation  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Tartaglia, James  
; APPLICANT: Cox, William I  
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus  
; FILE REFERENCE: 454310-2690.1  
; CURRENT APPLICATION NUMBER: US/09/136,159A  
; CURRENT FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: US 08/417,210  
; PRIOR FILING DATE: 1995-04-05  
; PRIOR APPLICATION NUMBER: US 08/223,842  
; PRIOR FILING DATE: 1994-04-06



; PRIOR APPLICATION NUMBER: US 07/897,382  
; PRIOR FILING DATE: 1992-06-11  
; PRIOR APPLICATION NUMBER: US 07/715,921  
; PRIOR FILING DATE: 1991-06-14  
; PRIOR APPLICATION NUMBER: US 08/105,483  
; PRIOR FILING DATE: 1993-08-12  
; PRIOR APPLICATION NUMBER: US 07/847,951  
; PRIOR FILING DATE: 1992-03-06  
; PRIOR APPLICATION NUMBER: US 07/713,967  
; PRIOR FILING DATE: 1991-06-11  
; PRIOR APPLICATION NUMBER: US 07/666,056  
; PRIOR FILING DATE: 1991-03-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 3807  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand  
US-09-136-159A-78

Query Match 52.1%; Score 1172.6; DB 4; Length 3807;  
Best Local Similarity 88.1%; Pred. No. 1.5e-280;  
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;

Qy	52	TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	1668	TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	1609
Qy	112	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA	171
Db	1608	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTA	1549
Qy	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACAT	231
Db	1548	TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGGCCACACAT	1489
Qy	232	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAAT	291
Db	1488	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGAATTGGTAAATGTGACAGAAAAAT	1429
Qy	292	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
Db	1428	TTTAAACATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGG	1369
Qy	352	GATGAAAGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCAC	411
Db	1368	GATCAAGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCAC	1309
Qy	412	AAATTG-----AATATCACTAAGAAATACTACTAATCCCACACTAGTAGCAGCTGG	459
Db	1308	GATTTGAGGAATACTACTAATACCAATAAATAGTACTGCTTAATAAACAATAAGTAAATAGCGAG	1249
Qy	460	GGATGATGGAGAAAGGAGAAATAAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGA	519
Db	1248	GGAAACAATAAAGGGAGGAGAAATGAAAAAAGTCTCTTTCAATATCACCACAAGCATAAGA	1189
Qy	520	AATAAGGTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAAAT	579
Db	1188	GATAAGATGCAGAAAGAAATATGCACCTCTTTATAAACTTGTATAGTATCAAT--AAAT	1132
Qy	580	ACTAATAATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGT	639
Db	1131	AATGATAGTACCAGCTATAGGTTGTATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT	1072
Qy	640	CCAAAGGTATCCTTTTCAGCCCAATCCCACATATTATTGTGCCGGCTGGTTTGGCATG	699
Db	1071	CCAAAGATATCCTTTGAGCCCAATCCCACATATTATTGTGCCCGGCTGGTTTGGCATT	1012
Qy	700	CTAAAGTGTAAACAATAAGACATTCGAATGGATCAGGACCATGCACAAAATGTCAGCACAGTA	759
Db	1011	CTAAAGTGTAAACGATAAAAAGTTTCAGTGGAAAAGGATCATGTGTAATAAATGTCAGCACAGTA	952

Qy	760	CAATGTACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTA	819
Db	951	CAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA	892
Qy	820	GCAGAAAGAAGACATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACCATAATA	879
Db	891	GCAGAAAGAAGAGGTAGTAATTAGATCTGAGAAATTTCAATGATAATGCTAAAAACCATATA	832
Qy	880	GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGA	939
Db	831	GTACATCTGAATGAATCTGTACAAAATTAATTGTACAAGACCCCAACTACAATAAAAGAAA	772
Qy	940	AGGTTATCTATAGGACCAGGGGAGAGCATTTTATGCAAGAAAGAAAACATAATAGGAGATATA	999
Db	771	AGGATACATATAGGACCAGGGGAGAGCATTTTATACAACAAAAAAATATAATAGGAACCTATA	712
Qy	1000	AGACAAAGCACATTGTAACATTAGTAGAGCAAAAATGGAATAAACACTTTTACAACAGATAGTT	1059
Db	711	AGACAAAGCACATTGTAACATTAGTAGAGCAAAAATGGAATGACACTTTTAAGACAGATAGTT	652
Qy	1060	ATAAAATTAAGAGAAAAATTTAGGAATAAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGG	1119
Db	651	AGCAAAATTAAGAGAACAAATTTAAGAAATAAAACAATAGTCTTTTAATCAATCCTCAGGAGGG	592
Qy	1120	GACCCAGAAAATTGTAATGGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAAATACA	1179
Db	591	GACCCAGAAAATTGTAATGGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAAATCA	532
Qy	1180	GCACAACTGTTTAAATAGTACTTGAATGTTACTTGGAGGGACAAAATGGCACGTGAAG--A	1236
Db	531	TCACCACCTGTTTAAATAGTACTTGAATGGTAATAATACTTGGAAATAATACTACAGGCTCA	472
Qy	1237	AATGACATAATCACACTCCAATGCAGAAATAAAACAATAATATAAATATGTGGCAGAAAGTA	1296
Db	471	AATAACAATATCACACTTCAATGCAAAATAAAACAATAATATAAACAATGTGGCAGGAAGTA	412
Qy	1297	GGAAAAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACA	1356
Db	411	GGAAAAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA	352
Qy	1357	GGGCTGCTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTTC	1413
Db	351	GGGCTACTATTTAACAAGAGATGGTGGTAAGGACACGGACAGAACGACACCGAGATCTTTC	292
Qy	1414	AGACCTGGAGGAGGAGATATAGGGGACAAATTGGAGAAAGTCAATTATATAAATATAAAGTA	1473
Db	291	AGACCTGGAGGAGGAGATATAGGGGACAAATTGGAGAAAGTCAATTATATAAATATAAAGTA	232
Qy	1474	GTAAGAATTTGAACCAATAGGAGTAGCACCCACCGAGGGCAAGAGAGAAACAGTGCAAAGA	1533
Db	231	GTAACAATTTGAACCAATTAGGAGTAGCACCCACCGAGGGCAAGAGAGAGTGGTGCAGAGA	172
Qy	1534	GAATAAAGA 1542	
Db	171	GAATAAAGA 163	

RESULT 8  
US-08-254-358-3  
; Sequence 3, Application US/08254358  
; Patent No. 5658785  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA





ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,391  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/254,358  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 578621land, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31975  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2571 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-475-391-3

Query Match 52.1%; Score 1172.4; DB 1; Length 2571;  
Best Local Similarity 88.2%; Pred. No. 1.4e-280;  
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;  
Qy 58 TCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117  
Db 40 TGGGATGGGCACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99  
Qy 118 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 177  
Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAAGAAGCAACCACTCTATTTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCATATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTGGGCCACACAAGCCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAATGTGACAGAAAAATTTTAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAAGAAGTAGAATTGGTAATGTGACAGAAAAATTTTAAC 279  
Qy 298 ATGTGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357  
Db 280 ATGTGAAAAATAACATGGTAGACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339  
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTCACATAATTG 417  
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTCACATAATTG 399  
Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAATAGCGAGGAACA 459  
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTTCTATATCACCACAAGCATAGAATAAAG 525  
Db 460 ATAAAGGAGGAGAAATGAAAAACTGCTCTTTTCAATATCACCACAAGCATAGAGATAAG 519  
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT 585

Db 520 ATGCAGAAAGAAATATGCACCTTCTTTATAAAACCTTGATATAGTATCAATAG--ATAATGAT 576  
Qy 586 AATACTAAGTATAGGTTAAATAGTTGTAAACACCTCAGTCATTACAGGCCTGTCCAAAG 645  
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAAG 636  
Qy 646 GTATCCTTTTCAGCCCAATTCCTCATACATTATTGTGTCGCGGCTGGGTTTTCGATGCTAAAG 705  
Db 637 ATATCCTTTGAGCCCAATTCCTCATACACTATTGTGCCCCGGCTGGTTTTCGATTCTAAAA 696  
Qy 706 TGTAAACAATAAGACATTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGT 765  
Db 697 TGTAAACGATAAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTCAGCACAGTACAATGT 756  
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTTAAATGGCAGTCTAGCAGAA 825  
Db 757 ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTTAAATGGCAGTCTAGCAGAA 816  
Qy 826 GAAGACATAGTAATTAGATCTGAAAAATTTTACAGACAATGCTAAAAACCATATAATAGTACAG 885  
Db 817 GAAGAGGTAGTAATTAGATCTGAGAATTTTCACTGTATAATGCTAAAAACCATCATAGTACAT 876  
Qy 886 CTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATAACAAGAAGAGGTTA 945  
Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAAGACCCCACTACAATAAAAGAAAAAGGATA 936  
Qy 946 TCTATAGGACCAGGGAGAGCATTTTATGCAAGAAGAAAACATAATAGGAGATATATAAGACAA 1005  
Db 937 CATATAGGACCAGGGAGAGCATTTTATACAACAACAAAAATATAATAGGAACATATAAGACAA 996  
Qy 1006 GCACATTGTAAACATTAGTAGACAAAAATGGAATAACACTTTACAACAGATAGTTTATAAAA 1065  
Db 997 GCACATTGTAAACATTAGTAGACAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056  
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCA 1125  
Db 1057 TTAAGAGAAACAATTTAAGAAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGGACCCA 1116  
Qy 1126 GAAATGTAAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTGTAAATACAGCACAA 1185  
Db 1117 GAAATGTAAATGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAAATACATCACCA 1176  
Qy 1186 CTGTTTAAATAGTACTTTGGAATG--TTACTGGAGGGACAAAATGGCACTGAAGGAAATGAC 1242  
Db 1177 CTGTTTAAATAGTACTTTGGAATGGAATAATACTTTGGAATAATACTACAGGGTCAAATAAC 1236  
Qy 1243 ATAATCACACTCCAATGCAGAATAAAACAAATTATATAATATGTGGCAGAAAAGTAGGAAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAA 1296  
Qy 1303 GCAATGTATGCCCCCTCCCATCA CAGGACAAAATTAGATGTTTCATCAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCCCTCCCATTTGAAGGACAAAATTAGATGTTTCATCAAATATTACAGGGCTA 1356  
Qy 1363 CTACTAAACAAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGTTGGTAAAGGACACGGACACGACACGACACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATTATATAATAATAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATTATATAATAATAAAGTAGTAACA 1476  
Qy 1480 ATTGAACCAATAGGAGTAGCACCACCCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAA 1539  
Db 1477 ATTGAACCATTAGGAGTAGCACCACCCCAAGGCAAGAGAGAGTGGTGCAGAGAGAAAAA 1536  
Qy 1540 AGAG 1543  
Db 1537 AGAG 1540

RESULT 10  
US-08-709-609-3

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; Sequence 3, Application US/08709609
; Patent No. 5858775
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858775and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-709-609-3

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Db	460	ATAAAGGGAGAGAAATGAAAAA	CTGCTCTTCAATATCACCACAAGCATAAGAGATAAG	519
Qy	526	GTAAAGAAAGAAATATGCAC	TTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT	585
Db	520	ATGACAGAAAGAAATATGCAC	TTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT	576
Qy	586	AATACTAAGTATAGGTTAATAA	AGTTGTAAACCTCAGTCATTACACAGGCCTGTCTCCAAAG	645
Db	577	AGTACCAGCTATAGGTTGATAA	GTGTAATACCTCAGTCATTACACAAGCTTGTCTCCAAAG	636
Qy	646	GTATCCTTTCAGCCAAATCCCA	TATATGTGTCCGGCTGGGTTTTCGGATGCTAAAG	705
Db	637	ATATCCTTTGAGCCAAATCCCA	TATACACTATTGTGCCCGGCTGGTTTTCGGATTCTAAAA	696
Qy	706	TGTAACAATTAAGACATTTCAAT	TGGATCAGGACCATGCACAAAATGTTCAGCACAGTACAATGT	765
Db	697	TGTAACGATAAAAAGTTT	CAGTGGAAAAGGATCATGTAAAAATGTTCAGCACAGTACAATGT	756
Qy	766	ACACATGGAATTAGGCCAGTGG	TGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	825
Db	757	ACACATGGAATTAGGCCAGTGG	TATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	816
Qy	826	GAAGACATAGTAATTAGATCTG	AAAAATTTACAGACAAATGCTAAAAACCATAATAGTACAG	885
Db	817	GAAGAGGTAGTAATTAGATCTG	AGAAATTTCACTGATAATGCTAAAAACCATCATAGTACAT	876
Qy	886	CTAAATGAATCTGTAGTAATTA	ATTGTTCAAGACCCCAACAATACAAAGAAAGGTTA	945
Db	877	CTGAATGAATCTGTACAAATTA	ATTGTTCAAGACCCCAACTACAATAAAAGAAAAGGATA	936
Qy	946	TCTATAGGACGAGGAGAGCAT	TTTTTATGCAAGAAGAAAACATATAGGAGATATAAGACAA	1005
Db	937	CATATAGGACGAGGAGAGCAT	TTTTTATACAAAAAAAATATATAGGAACTATAAGACAA	996
Qy	1006	GCACATTGTAACATTAGTAGAG	CAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAA	1065
Db	997	GCACATTGTAACATTAGTAGAG	CAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAA	1056
Qy	1066	TTAAGAGAAAAATTTAGGAATA	AAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA	1125
Db	1057	TTAAAAGAACAAATTAAGAA	TAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA	1116
Qy	1126	GAAATTGTAATGCACAGTTT	TAAATTGTGAGGGGAATTTCTTCTACTGTATAACAGCACAA	1185
Db	1117	GAAATTGTAATGCACAGTTT	TAAATTGTGAGGGGAATTTTCTACTGTATAACATCACCA	1176
Qy	1186	CTGTTTAAATAGTACTTGGAA	TG--TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC	1242
Db	1177	CTGTTTAAATAGTACTTGGAA	TGGTAATAACTTTGGAATAATACTACAGGCTCAATAAC	1236
Qy	1243	ATAATCACACTCCAAATGCAGA	ATAAAAAATTATAAATATGTGGCAGAAAAGTAGGAAAA	1302
Db	1237	AATATCACACTTCAATGCRAA	ATAAAAAATTATAAACAATGTGGCAGGAAGTAGGAAAA	1296
Qy	1303	GCAATGTATGCCCTCCCATCAC	AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG	1362
Db	1297	GCAATGTATGCCCTCCCATTGA	AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA	1356
Qy	1363	CTACTAACAGAGATGGAGGTA	ATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT	1419
Db	1357	CTATTAAACAAGAGATGGTGT	AAGGACCGACACGACCCGAGATCTTCAGACCT	1416
Qy	1420	GGAGGAGGAGATATGAGGGACA	ATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGA	1479
Db	1417	GGAGGAGGAGATATGAGGGACA	ATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAACA	1476
Qy	1480	ATTGAACCAATAGGAGTAGCAC	CCCCCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAA	1539
Db	1477	ATTGAACCAATAGGAGTAGCAC	CCCCCAGGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAA	1536
Qy	1540	AGAG	1543	



Db 1537 AGAG 1540

RESULT 11

US-09-552-950-3

; Sequence 3, Application US/09552950

; Patent No. 6541248

; GENERAL INFORMATION:

; APPLICANT: Oxford Biomedica (UK) Limited

; TITLE OF INVENTION: Anti-Viral Vectors

; FILE REFERENCE: 674524-2004

; CURRENT APPLICATION NUMBER: US/09/552,950

; CURRENT FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2571

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-09-552-950-3

Query Match 52.1%; Score 1172.4; DB 4; Length 2571;

Best Local Similarity 88.2%; Pred. No. 1.4e-280;

Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

QY 58 TCGGCTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117

Db 40 TGGGATGGGCACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99

QY 118 TGGGTACAGTCTATTATGGGTPACCTGTGTGGAGAGAGCAACCACCCTCTATTTTGT 177

Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAAAGRAGCAACCACCCTCTATTTTGT 159

QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 237

Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAAGCCTGT 219

QY 238 GTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAC 297

Db 220 GTACCCACAGACCCCAACCCACAAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTTAAC 279

QY 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATAPAAATCAGTTTATGGGATGAA 357

Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339

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RESULT 12

US-09-936-572-3

; Sequence 3, Application US/09936572

; Patent No. 6783981

; GENERAL INFORMATION:

; APPLICANT: UDEN, MARK

; APPLICANT: MITROPHANOUS, KYRIACOS

; TITLE OF INVENTION: ANTI-VIRAL VECTORS

; FILE REFERENCE: 078883/0137

; CURRENT APPLICATION NUMBER: US/09/936,572

; CURRENT FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: PCT/GB00/01002

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: GB 9906177.2

; PRIOR FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 73





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; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-07178-3

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; Sequence 66, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1222.2	54.3	9540	17	US-10-325-468-46 Sequence 46, Appl
2	1198	53.2	2612	15	US-10-414-692-20 Sequence 20, Appl
3	1197	53.2	1512	9	US-09-759-841-3 Sequence 3, Appli
4	1179.8	52.4	1422	18	US-10-728-195-7 Sequence 7, Appli
5	1172.6	52.1	3807	15	US-10-441-788-78 Sequence 78, Appl
6	1172.4	52.1	2571	9	US-09-999-183-3 Sequence 3, Appli
7	1172.4	52.1	2571	13	US-10-077-294-3 Sequence 3, Appli
8	1172.4	52.1	2571	13	US-10-163-886-3 Sequence 3, Appli
9	1172.4	52.1	2571	14	US-10-263-127-3 Sequence 3, Appli
10	1172.4	52.1	2571	15	US-10-375-777-3 Sequence 3, Appli
11	1172.4	52.1	2571	16	US-10-351-938-3 Sequence 3, Appli
12	1171.8	52.0	2552	10	US-09-966-931-27 Sequence 27, Appl

13	1171.8	52.0	2552	17	US-10-459-121-27	Sequence 27, Appl
14	1168.6	51.9	2573	10	US-09-966-931-29	Sequence 29, Appl
15	1168.6	51.9	2573	17	US-10-459-121-29	Sequence 29, Appl
16	1166.6	51.8	9715	17	US-10-325-468-44	Sequence 44, Appl
17	1165.6	51.8	9706	17	US-10-325-468-45	Sequence 45, Appl
18	1165.4	51.7	9704	17	US-10-325-468-40	Sequence 40, Appl
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20	1165.4	51.7	9942	17	US-10-325-468-54	Sequence 54, Appl
21	1164.4	51.7	2627	15	US-10-177-390-9	Sequence 9, Appli
22	1162.2	51.6	9737	10	US-09-827-688-12	Sequence 12, Appl
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25	1162.2	51.6	9942	17	US-10-325-468-7	Sequence 7, Appli
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32	1160.8	51.5	1929	14	US-10-032-162-12	Sequence 12, Appl
33	1160.6	51.5	9942	17	US-10-325-468-3	Sequence 3, Appli
34	1160.6	51.5	9942	17	US-10-325-468-52	Sequence 52, Appl
35	1160.4	51.5	2570	10	US-09-966-931-31	Sequence 31, Appl
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39	1158.4	51.4	1530	15	US-10-361-849-13	Sequence 13, Appl
40	1150.6	51.1	2214	15	US-10-336-566-85	Sequence 85, Appl
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44	1150.6	51.1	9544	15	US-10-336-566-7	Sequence 7, Appli
45	1150.6	51.1	9545	17	US-10-093-953A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

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; Sequence 46, Application US/10325468  
; Publication No. US20040101823A1  
; GENERAL INFORMATION:  
; APPLICANT: Soong, Nay Wei  
; APPLICANT: Pekrun, Katja  
; APPLICANT: Shibata, Riri  
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL  
; FILE REFERENCE: 0166.210US  
; CURRENT APPLICATION NUMBER: US/10/325,468  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/343,524  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
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; ORGANISM: Human immunodeficiency virus 1  
; FEATURE:  
; OTHER INFORMATION: parent JRCSEF DNA (GenBank Accession No. M38429)  
US-10-325-468-46

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Best Local Similarity 90.3%; Pred. No. 1.3e-275;  
Matches 1334; Conservative 0; Mismatches 128; Indels 15; Gaps 2;

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Qy 1094 TAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTTGAATGCACAGTTTAAATTGTG 1153

Db 7299 TAGTCTTTACTCACTCCTCAGGAGGGATCCAGAAAATTTGAATGCACAGTTTAAATTGTG 7358

Qy 1154 GAGGGAATTTCTTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAATGTTACTG 1213

Db 7359 GAGGGAATTTTCTACTGTAATTC AACACAACTGTTTAAATAGTACTTTGGAATGATACTG 7418

Qy 1214 GAGGGAATAATGGCACTGAAGGNAATGACATAATCACACTCCAATGCAGAAATAAAACAAA 1273

Db 7419 AAAAGTCAAGTGGCACTGAAGGAAATGACACCATCATACTCCCATGCAGAAATAAAACAAA 7478

Qy 1274 TTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCCCTCCCATCACAGGACAAA 1333

Db 7479 TTATAAACATGTGGCAGGAAGTGGGAAAAGCAATGTATGCTCCTCCCATTTAAAGGACAAA 7538

Qy 1334 TTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAGTACTG 1393

Db 7539 TTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTAA---AAATG 7595

Qy 1394 AGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAATTTGGAGAAAGTG 1453

Db 7596 AGAGTGAGATCGAGATCTTCAGACCTGGAGGAGGAGACATGAGGGACAATTTGGAGAAAGTG 7655

Qy 1454 AATTATATAAATATAAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCCACCAGGCAAA 1513

Db 7656 AATTATATAAATATAAAGTAGTAAAAATTTGAACCAATTAGGAGTAGCACCCACCAGGCAA 7715

Qy 1514 AGAGAAGAACAGTGCAAAAGAGAAAAAAGAGGGGGAGG 1550

Db 7716 AGAGAAGAGTGGTGCAAGAGAAAAAAGAGCAGTGGG 7752

RESULT 2

US-10-414-692-20  
; Sequence 20, Application US/10414692  
; Publication No. US20030228607A1  
; GENERAL INFORMATION:  
; APPLICANT: X-Septor Therapeutics, Inc.  
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic  
; TITLE OF INVENTION: profile  
; FILE REFERENCE: 8012-002-US  
; CURRENT APPLICATION NUMBER: US/10/414,692  
; CURRENT FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: 60/372,650  
; PRIOR FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 2612  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-414-692-20

Query Match 53.2%; Score 1198; DB 15; Length 2612;  
Best Local Similarity 90.6%; Pred. No. 3.4e-270;  
Matches 1341; Conservative 0; Mismatches 115; Indels 24; Gaps 5;

Qy 74 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTGTGGTCCACAGTCTATT 133

Db 450 TGCTCCTTGGGATATTAAATGATCTGTAGTGTCTGTAGAAAAGTTGTGGTCCACAGTCTATT 509

Qy 134 ATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACCTCTATTTTTGTGCATCAGATGCTAAAG 193

Db 510 ATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACCTCTATTTTTGTGCATCAGATGCTAAAG 569

Qy 194 CCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCA 253

Db 570 CATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCA 629

Qy 254 ACCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 313

Db 630 ACCACAAGAAAGTAGTATTGGAAAAATGTAAACAGAACATTTTAAACATGTGGAAAAATAACA 689

Qy 314 TGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAAAGCCTTAAAGCCATGTG 373

Db 690 TGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGATCAAAAGCCTTAAAGCCATGTG 749

Qy 374 TAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCCTAATTTGAATATCACTAAGAATA 433

Db 750 TAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCAAGGATGT-----GAATG 797

Qy 434 CTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATAAAAAATTGCT 493



Db 798 CTACTAATACCACCTAATGATAGCGAGGGAACGATGGAGAGAGGAGAAATAAAAACTGCT 857

Qy 494 CTTTCTATATCACCACAAGCATAGAATAAAGGTAAAGAAAGAAATATGCACCTTTTAAATA 553  
|||||

Db 858 CTTTCAATATCACCACAAGCATAGAAGATGAGGTGCAGAAAGAATATGCTCTTTTATA 917  
|||||

Qy 554 GACITGATGTAGTACCAATAGAAAATACTAATAATACTAAGTATAGGTTAATAAGTTGTA 613  
|||||

Db 918 AACITGATGTAGTACCAATAG---ATAATAATAATACCAGCTATAGGTTGATAAGTTGTG 974  
|||||

Qy 614 ACACCTCAGTCATTACACAGGCTGTCTCCAAAGGTATCCTTTCAGCCAATTCCCATACAATT 673  
|||||

Db 975 ACACCTCAGTCATTACACAGGCTGTCTCCAAAGATATCCTTTGAGCCAATCCCATACAATT 1034  
|||||

Qy 674 ATTGTGTCCGGCTGGGTTTGGCATGCTTAAAGTGTAACAATAAGACATTCAATGGATCAG 733  
|||||

Db 1035 ATTGTGCCCGCTGGTTCGCGATTCTAAAGTGTAATGATAAGACGTTCAATGGAAAG 1094  
|||||

Qy 734 GACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGGTGCAA 793  
|||||

Db 1095 GACCATGTAAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTAGTATCAA 1154  
|||||

Qy 794 CTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAGACATAGTAATTAGATCTGAAAATT 853  
|||||

Db 1155 CTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAGAGGTAGTAATTAGATCTGACAAATT 1214  
|||||

Qy 854 TCACAGACAAATGCTAAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTAATTGTA 913  
|||||

Db 1215 TCAGGAACAATGCTAAAACCAATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTA 1274  
|||||

Qy 914 CAAGACCCAAACAATAACAGAAGAAGGTTATCTATAGGACCAGGGAGAGCATTTTATG 973  
|||||

Db 1275 CAAGACCCAAACAATAACAGAAAAAAGTATACATATAGGACCAGGGAGAGCATTTTATA 1334  
|||||

Qy 974 CAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTGAACATTAGTAGAGCAAAAT 1033  
|||||

Db 1335 CTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTGAACATTAGTAGAGCAAAAT 1394  
|||||

Qy 1034 GGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGAGAAAAATTTAGGAATAAAACAA 1093  
|||||

Db 1395 GGAATGACACTTTTAAAACAGATAGTTATAAAATTAAGAGAACAAATTTGAGAAATAAAACAA 1454  
|||||

Qy 1094 TAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTGTAATGCACAGTTTTTAATTGTG 1153  
|||||

Db 1455 TAGTCTTTAATCACTCCTCAGAGGGGACCCAGAAATTGTAATGCACAGTTTTTAATTGTG 1514  
|||||

Qy 1154 GAGGGGAATTCTTCTACTGTATAACAGCACAACTGTTTAAATAGTACTTGG---AATGTTA 1210  
|||||

Db 1515 GAGGAGAAATTTTCTACTGTAAATCAACACAACACTGTTTAAATAGTACTTGGAAATAATA 1574  
|||||

Qy 1211 CTGGAGGGACAATAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAGAATAAAAC 1270  
|||||

Db 1575 CTGAAGGTCAAATAACACTGAAGGAAT--ACTATCACACTCCCATGCAGAATAAAAC 1631  
|||||

Qy 1271 AAATTATAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGGAC 1330  
|||||

Db 1632 AAATTATAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATCAGAGGAC 1691  
|||||

Qy 1331 AAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAGAGATGGAGGTAATAGTA 1390  
|||||

Db 1692 AAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG---TATTA 1748  
|||||

Qy 1391 CTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAA 1450  
|||||

Db 1749 ATGAGAAATGGACCGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAA 1808  
|||||

Qy 1451 GTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCACGAGG 1510  
|||||

Db 1809 GTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCACCAAGG 1868  
|||||

Qy 1511 CAAAGAGAAGAACAGTGCAAAAGAGAAAAAGAGGGGGAGG 1550  
|||||

Db 1869 CAAAGAGAAGAGTGGTGCAAGAGAGAAAAAGAGCAGTGGG 1908  
|||||

RESULT 3

US-09-759-841-3  
; Sequence 3, Application US/09759841  
; Patent No. US20010039026A1  
; GENERAL INFORMATION:  
; APPLICANT: Rickett, Graham A  
; APPLICANT: Dobbs, Susan  
; APPLICANT: Perros, Manoussos  
; TITLE OF INVENTION: Assay Method  
; FILE REFERENCE: PC10348APME  
; CURRENT APPLICATION NUMBER: US/09/759,841  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1512  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-759-841-3

Query Match 53.2%; Score 1197; DB 9; Length 1512;  
Best Local Similarity 89.2%; Pred. No. 4.5e-270;  
Matches 1316; Conservative 0; Mismatches 150; Indels 9; Gaps 2;

Qy 74 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTGTGGTCACAGTCTATT 133  
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Db 38 TGCTGTGTGGAGCAGTCTTCGTTTCGGCTAGCGTAGAAAAATTTGTGGTCACAGTTTATT 97  
|||

Qy 134 ATGGGGTACCTGTGTGGAGAAAGCAACCACCACCTCTATTTTTGTGCATCAGATGCTAAAG 193  
|||||

Db 98 ATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACCTCTATTTTTGTGCATCAGATGCTAAAG 157  
|||||

Qy 194 CCTATGATACAGAGGTACATAATGTTTGGGGCCACAGATGCCTGTGTACCCACAGACCCCA 253  
|||||

Db 158 CATATGATACAGAGGTACATAATGTTTGGGGCCACACATGCCTGTGTACCCACAGACCCCA 217  
|||||

Qy 254 ACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 313  
|||||

Db 218 ACCCACAAGAAGTAGAATTTGAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 277  
|||||

Qy 314 TGGTAGATCAGATCAGGATATAATCAGTTTATGGATGAAAGCCTAAAGCCATGTG 373  
|||||

Db 278 TGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGATCAAAGCCTAAAGCCATGTG 337  
|||||

Qy 374 TAAAAATTAACCCCACTCTGTGTACTTTTAAATTGCACATAATTGA-----ATATCACA 427  
|||||

Db 338 TAAAAATTAACCTCCACTCTGTGTACTTTTAAATTGCACATGATTGAGGAATGCTACTAATG 397  
|||||

Qy 428 AGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAATAAAA 487  
|||||

Db 398 GGAATGACACTAATACCACACTAGTAGTAGCAGGGGAATGATGGGGGGAGGAGAAATGAAA 457  
|||||

Qy 488 ATTGCTCTTTCTATATACCAACAAGCATAGAATAAGGTAAGGTAAGAAAGAAATATGCATTT 547  
|||||

Db 458 ATTGCTCTTTTCAAAATACCACAAAAACATAAGAGGTAAAGGTGCAGAAAGAAATATGCATTT 517  
|||||

Qy 548 TTAATAGACTTGATGTAGTACCAATAGAAAAATCTAATAATCTAAGTATAGGTTAATAA 607  
|||||

Db 518 TTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAATAATAGATATAGGTTGATAA 577  
|||||

Qy 608 GTTGTAAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTTTCAGCCCAATTCOCA 667  
|||||

Db 578 GTTGTAAACACCTCAGTCATTACACAGGCCCTGTCCAAAGATATCCTTTTTCAGCCCAATTCOCA 637  
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Qy 668 TACATTATTGTGTCCCGCTGGGTTTTCGGATGCTAAAGTGTAAACAATAAGACATTTCATG 727  
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Db  TACATTATTGTCCTCCGGCTGGTTTTCGGAATCTTAAAGTGTAAAGATAAGAAGTTCAATG 697
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QY  GATCAGGACCATGCACAAATGTCAGCACAGTACAATGTFACACATGGAATTAGGCCAGTGG 787
|||
Db  GAAAAGGACCATTGTTCAAATGTCAGCACAGTACAATGTFACACATGGGATTAGGCCAGTAG 757
|||||
QY  TGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTAGATCTG 847
|||||
Db  TATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAGGTAGTAATTAGATCCG 817
|||||
QY  AAAATTTACAGACAATGCTTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAATTA 907
|||||
Db  AAAATTTGCGGACAATGCTTAAACCATAATAGTACAGCTGAATGAATCTGTAGAAATTA 877
|||||
QY  ATTGTACAAGACCCCAACAATAACAAGAAGAGTTATCTATAGGACCCAGGGAGACCAT 967
|||||
Db  ATTGTACAAGACCCCAACAATAACAAGAAAAAGTATACATATAGGACCCAGGCAGACAT 937
|||||
QY  TTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAGAG 1027
|||||
Db  TATATACAACAGGAGAAATAATAGGAGATATAGACAAGCACATTGTAACCTTAGTAGAG 997
|||||
QY  CAAAATGGAATAACACTTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATA 1087
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Db  CAAAATGGAATGACACTTTTAAATAAGATAGTTTATAAAATTAAGAGAACAAATTTGGGAATA 1057
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QY  AAACAATAGCCTTTAAGCATTCTCAGGAGGGGCCCAAGAAATGTAATGCACAGTTTTA 1147
|||||
Db  AAACAATAGTCTTTAAGCATTCTCAGGAGGGGCCCAAGAAATGTAATGCACAGTTTTA 1117
|||||
QY  ATTGTGGAGGGGAATTTCTTCTACTGTTAATACAGCACAACTGTTTAAATAGTACTTGGAAATG 1207
|||||
Db  ATTGTGGAGGGGAATTTTCTTCTACTGTTAATCAACACAACTGTTTAAATAGTACTTGGAAATG 1177
|||||
QY  TTAAGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1267
|||||
Db  TTAAGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1237
|||||
QY  AACAAATTATAAATATGTGGCAAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAG 1327
|||||
Db  AACAAATTATAAATATGTGGCAAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAG 1297
|||||
QY  GACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTCCCG 1387
|||||
Db  GACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTCCCG 1357
|||||
QY  GTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGA 1447
|||||
Db  AGGCCAACA---AGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGA 1414
|||||
QY  GAAGTGAATTATATAAATATAAAGTAGTAAAGAAATTGAACCAATTAGGAGTAGCACCCACCA 1507
|||||
Db  GAAGTGAATTATATAAATATAAAGTAGTAAAGAAATTGAACCAATTAGGAGTAGCACCCACCA 1474
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QY  GGGCAAGAGAGAAGAACAGTGCAAAGAGAAAAAAGA 1542
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Db  AGGCAAGAGAGAAGAGTGGTGCAGAGAGAAAAAAGA 1509
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RESULT 4
US-10-728-195-7
; Sequence 7, Application US/10728195
; Publication No. US20040191269A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Shan
; APPLICANT: Pal, Ranajit
; APPLICANT: Kalyanaraman, V.S.
; APPLICANT: Whitney, Stephen Charles
; APPLICANT: Keen, Tim
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS
; FILE REFERENCE: 07917-269001
```

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; CURRENT APPLICATION NUMBER: US/10/728,195
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/430,732
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-728-195-7

Query Match      52.4%; Score 1179.8; DB 18; Length 1422;
Best Local Similarity 90.4%; Pred. No. 4.8e-266;
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

QY 115 TTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTATTT 174
Db 1 TTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTATTT 60

QY 175 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCC 234
Db 61 TGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCC 120

QY 235 TGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTT 294
Db 121 TGTGTACCCACAGACCCCAACCCACAAGAAGTAGAATTGGAAAAATGTGACAGAAAAATTT 180

QY 295 AACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGAT 354
Db 181 AACATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGAT 240

QY 355 GAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTCGACTAAT 414
Db 241 CAAAGCCTAAAGCCATGTGTAAAAATTAACCTCCACTCTGTGTACTTTAAATTCGACTGAT 300

QY 415 TTGA-----ATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATG 468
Db 301 TTGAGGAATGCTACTAATGGGAATGACACTAATACCCTAGTAGTAGCAGGGAAATGATG 360

QY 469 GAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACACAAGCATAAAGAAATAAGGTA 528
Db 361 GGGGAGGAGAAATGAAAAATTTGCTCTTTCAAAATCACACAACATAAGAGGTAAGGTG 420

QY 529 AAGAAAGAAATATGCACITTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAAT 588
Db 421 CAGAAAGAAATATGCACITTTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAAT 480

QY 589 ACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTA 648
Db 481 AATAGATATAGGTTTGATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGATA 540

QY 649 TCCTTTCAGCCAATTCCTATACATTATTGTGTCCCGCTGGGTTTTCGATGCTAAAGTGT 708
Db 541 TCCTTTGAGCCAATTCCTATACATTATTGTGCCCGCTGGTTTTTCGATTCCTAAAGTGT 600

QY 709 AACAAATAAGACATTCATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACA 768
Db 601 AAAGATAAGAAGTTCAATGGAAGAGGACCATGTTCAAATGTGAGCACAGTACAATGTACA 660

QY 769 CATGGAATTAGGCCAGTGGTGTCAAACCTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAA 828
Db 661 CATGGATTAGGCCAGTAGTATCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAA 720

QY 829 GACATAGTAATTAGATCTGAAAAATTTACAGACAATGCTTAAACCATAATAGTACAGCTA 888
Db 721 GAGGTAGTAATTAGATCCGAAAAATTTGCGGACAATGCTTAAACCATAATAGTACAGCTG 780

QY 889 AATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAATAACAAGAAAGGTTTATCT 948
Db 781 AATGAATCTGTAGAAATTAATTGTACAAGACCCCAACAATAACAAGAAAGTATACAT 840

QY 949 ATAGGACGAGGAGAGCAATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCA 1008
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Db      841 ATAGGACCGCAGAGCAATTATATACAACAGGAGAAATAATAGGAGATATAAGACAAGCA 900
Qy      1009 CATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAATTA 1068
Db      901 CATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTA 960
Qy      1069 AGAGAAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCAGAA 1128
Db      961 AGAGAACAAATTTGGGAATAAAACAATAGTCTTTAAGCATTCCTCAGGAGGGACCCAGAA 1020
Qy      1129 ATTGTAATGCACAGTTTAAATTGTGAGGGGAATTCTTCTACTGTAAATACAGCACAACTG 1188
Db      1021 ATTGTACGCACAGTTTAAATTGTGAGGGGAATTTTCTACTGTAAATCAACACAACTG 1080
Qy      1189 TTTAATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATC 1248
Db      1081 TTTAATAGTACTTGGAAATGTTACTGAAGAGTCAAATAACACTGTAGAAAATAACACAATC 1140
Qy      1249 AACTCCCAATGCAGAAATAAAACAATTAATAATATGTGGCAGAAAAGTAGGAAAAGCAATG 1308
Db      1141 AACTCCCAATGCAGNAATAAAACAATTAATAACATGTGGCAGAAAAGTAGGAGAGCAATG 1200
Qy      1309 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTA 1368
Db      1201 TATGCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTATTA 1260
Qy      1369 ACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGA 1428
Db      1261 ACAAGAGATGGTGGTCCAGAGGCAACA---AGACCGAGGTCTTCAGACCTGGAGGAGGA 1317
Qy      1429 GATATGAGGGACAATTTGGAGAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCA 1488
Db      1318 GATATGAGGGACAATTTGGAGAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCA 1377
Qy      1489 ATAGGAGTAGCACCCACCAGGCAAGGCAAGAGAAAGAACAGTGC 1529
Db      1378 TTAGGAGTAGCACCCACCAGGCAAGGCAAGAGAGAGTGGTGA 1418
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RESULT 5
US-10-441-788-78/c
; Sequence 78, Application US/10441788
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/10/441,788
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/136,159A
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-10-441-788-78
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Query Match      52.1%; Score 1172.6; DB 15; Length 3807;
Best Local Similarity 88.1%; Pred. No. 3.7e-264;
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;
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Qy      52 TGGATCTCGGCTTCGAGATCTATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAA 111
Db      1668 TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609
Qy      112 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCACACTCTA 171
Db      1608 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAAAGAAGCAACCACACTCTA 1549
Qy      172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db      1548 TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489
Qy      232 GCCTGTGTACCCACAGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAAT 291
Db      1488 GCCTGTGTACCCACAGACCCCAACCCACAAGAAAGTAGAATTGGTAAATGTGACAGAAAAAT 1429
Qy      292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTTATGG 351
Db      1428 TTTAACATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTTATGG 1369
Qy      352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCAC 411
Db      1368 GATCAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCAC 1309
Qy      412 AATTG-----AATATCACTAAGAATACTACTAATCCCACTAGTCCCACTAGTGCAGCTGG 459
Db      1308 GATTGAGGAATACTACTAATAACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGAG 1249
Qy      460 GGAATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTCTATATCACCACAAGCATAGA 519
Db      1248 GGAACAATAAAGGGAGGAGAAATGAAAAAATCTGCTCTTTCAATATCACCACAAGCATAGA 1189
Qy      520 AATAAGGTAAAGAAAGATATGCACCTTTTAAATAGACTTGTATGATGTAGTACCAATAGAAAAAT 579
Db      1188 GATAAGATGCAGAAAGAAATATGCACCTCTTTATAAACTTGATATAGTATCAAT---AAAT 1132
Qy      580 ACTAATAATACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGT 639
Db      1131 AATGATAGTACCAGCTATAGGTTGATAAGTTGTAAATACCTCAGTCATTACACAAGCTTGT 1072
Qy      640 CCAAAGGTATCCTTTTCAGCCAAATTCCTCATACATTATTGTGTCCCGGCTGGTTCGCGATG 699
Db      1071 CCAAAGATATCCTTTTGAGCCAATTCCTCATACACTATTGTGCCCCGGCTGGTTCGCGATT 1012
Qy      700 CTAAAGTGTAACAATAAGACATTCAATGGATCAGGACCAATGCACAAATGTCAGCACAGTA 759
Db      1011 CTAAAGTGTAACGATAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTCAGCACAGTA 952
Qy      760 CAATGTACACATGGAAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTA 819
Db      951 CAATGTACACATGGAAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA 892
Qy      820 GCAGAAAGACATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACCATAATA 879
Db      891 GCAGAAAGAGAGGTAGTAATTAGATCTGAGAAATTTCAATGATAATGCTAAAAACCATCATA 832
Qy      880 GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAATAACAAGAAGA 939
Db      831 GTACATCTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAGAAAA 772
Qy      940 AGGTTATCTATAGGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATA 999
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QY	1186	CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGGCAAAATGGCACTGAAGGAAATGAC	1242
DB	1177	CTGTTTAAATAGTACTTGGAAATGTTGGAAATAATACTACAGGGTCAAAATAAC	1236
QY	1243	ATAATCACACTCCCAATGCAGAAATAAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAAAA	1302
DB	1237	AATATCACACTTCAATGCAAAAATAAAAACAAATTATAAACAATGTGGCAGGAAGTAGGAAAA	1296
QY	1303	GCAATGTATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG	1362
DB	1297	GCAATGTATGCCCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA	1356
QY	1363	CTACTAAACAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT	1419
DB	1357	CTATTAAACAAGAGATGGTGTAGGACACCGGACACGACGACACCCGAGATCTTCAGACCT	1416
QY	1420	GGAGGAGGAGATATGCGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGA	1479
DB	1417	GGAGGAGGAGATATGCGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAACA	1476
QY	1480	ATTGAAACCAATAGGAGTAGCACCCACCGGGCAAAGAGAAGAAACAGTGCAGAGAGAAAAA	1539
DB	1477	ATTGAAACCAATTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAA	1536
QY	1540	AGAG	1543
DB	1537	AGAG	1540

## RESULT 7

US-10-077-294-3  
; Sequence 3, Application US/10077294  
; Publication No. US20020159979A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/077,294  
; FILING DATE: 15-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/691,604  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020159979A1and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:



Db 877 CTGAATGAATCTGTACAAATTAAATTGTACAAGACCCCAACTACATAAAAAAGGATA 936  
Qy 946 TCTATAGGACGAGGAGAGCATTTTATGCAAGAAGAAACATATAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACGAGGAGAGCATTTTATACAACAATAATATAAGAACTATAAGACAA 996  
Qy 1006 GCACATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAA 1065  
Db 997 GCACATTGTAACATTAGTAGAGCAAAATGGAATGACACTTTAAGACAGATAGTTAGCAA 1056  
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCA 1125  
Db 1057 TTAAGAGAACAAATTTAAGAAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116  
Qy 1126 GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTACTGTAATACAGCACAA 1185  
Db 1117 GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176  
Qy 1186 CTGTTTAATAGTACTTGGAATG---TACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242  
Db 1177 CTGTTTAATAGTACTTGGAATGGTAATAATACTTTGGAATAATACTACAGGGTCAAATAAC 1236  
Qy 1243 ATAATCACACTCCAATGCAGAATAAAACAAATTATATAATATCTGGCAGAAAGTAGGAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAA 1296  
Qy 1303 GCAATGTATGCCCCCTCCCATCACAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCCCTCCCATTTGAAGACAAATTAGATGTTCAATCAAAATATTACAGGGCTA 1356  
Qy 1363 CTACTAACAAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGGACACGACGACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAATATAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAATATAAAGTAGTAACA 1476  
Qy 1480 ATTGAACCAATAGGAGTAGCACCCACCGGGCAAAGAGAAAGAACAGTGCAAAGAGAAAAA 1539  
Db 1477 ATTGAACCAATTAGGAGTAGCACCCACCAAGGCAAAGAGAAAGAGTGGTGCAGAGAGAAAA 1536  
Qy 1540 AGAG 1543  
Db 1537 AGAG 1540

RESULT 9

US-10-263-127-3  
; Sequence 3, Application US/10263127  
; Publication No. US20030082145A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/263,127  
; FILING DATE: 02-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,294  
; FILING DATE: 15-Feb-2002  
; APPLICATION NUMBER: 09/691,604  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20030082145Aland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-263-127-3

Query Match 52.1%; Score 1172.4; DB 14; Length 2571;  
Best Local Similarity 88.2%; Pred. No. 3.4e-264;  
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;  
Qy 58 TGGCTTCGAGATCTATGCTCTCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTG 117  
Db 40 TGGGATGGGCACGATGCTCTTGGGTTATTAAATGATCTGTAGTCTACAGAAAAATTG 99  
Qy 118 TGGTTCACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTTTGT 177  
Db 100 TGGTTCACAGTCTATTATGGGTACCTGTGTGGAAAGAAAGCAACCACTCTATTTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTGGGCCACACAGCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAATGTGACAGAAAAATTTTAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAAGAGTAGAATTGGTAAATGTGACAGAAAAATTTTAAC 279  
Qy 298 ATGTGGAAAAATAACATGTTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGA 357  
Db 280 ATGTGGAAAAATAACATGTTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCA 339  
Qy 358 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTGTACTTTAAATTCACATAATTG 417  
Db 340 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTGTACTTTAAATTCACATAATTG 399  
Qy 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
Db 400 AGGAATACTACTAATAATACCAATAATAGTACTGCTAATAACAATAAGTAATAGCGAGGAACA 459  
Qy 466 ATGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAG 525  
Db 460 ATAAAGGGAGGAGAAATGAAAACTGCTCTTTCAATATCACCACAAGCATAAAGAGATAAG 519  
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATACTAAT 585  
Db 520 ATGCAGAAAGAAATATGCACCTCTTTATAAAACCTTGATATAGTATCAATAG---ATAATGAT 576  
Qy 586 AATACTAAGTATAGGTTAATAAAGTTGTAACACCTCAGTCAATTACAGGCCTGTCCAAAG 645  
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCAATTACACAAGCTTTGTCCAAAG 636  
Qy 646 GTATCCTTTTCAGCCCAATCCCATACATTTATTGTGTCCCGGTGGGTTTTCGATGCTAAAG 705  
Db 637 ATATCCTTTGAGCCCAATTCCTCATACACTATTGTGCCCCGGCTGGTTTTCGATTTCTAAA 696  
Qy 706 TGTAAACAATAAGACATTTCAATGGATCAGGACCATGCACAATATGTACACAGTACAATGT 765  
Db 697 TGTAAACGATAAAAAAGTTTCAGTGGAAAAAGGATCATGTAAAAATGTACAGCACAGTACAATGT 756



QY	766	ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	825
DB	757	ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	816
QY	826	GAAGACATAGTAATTAGATCTGAAAAATTTCAACAGACAAATGCTAAAAACCATATAATAGTACAG	885
DB	817	GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGTATAATGCTAAAAACCATCATAGTACAT	876
QY	886	CTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCAAACAATACAGAAGAAGGTTA	945
DB	877	CTGAATGAATCTGTACAAAATTAATTTGTACAAGACCCAACTACAATAAAAGAAAAGGATA	936
QY	946	TCTATAGGACCAGGAGAGCATTTTATGCAAGAGAAAAACATAATAGGAGATATAAGACAA	1005
DB	937	CATATAGGACCAGGAGAGCATTTTATACAACAAAAATATAATAGGAACATATAAGACAA	996
QY	1006	GCACATTGTAACATTAGTAGAGCAAAAATGGAATAACACTTTACAACAGATAGTTATATAAA	1065
DB	997	GCACATTGTAACATTAGTAGAGCAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA	1056
QY	1066	TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA	1125
DB	1057	TTAAAAGAACAAATTTAAGAAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA	1116
QY	1126	GAAATTGTAATGCACAGTTTAAATGTGGAGGGGAATCTTCTACTGTAATACAGCACAA	1185
DB	1117	GAAATTGTAATGCACAGTTTAAATGTGGAGGGGAATTTTCTACTGTAATAATCATCACA	1176
QY	1186	CTGTTTAAATAGTACTTTGGAATG--TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC	1242
DB	1177	CTGTTTAAATAGTACTTTGGAATGTTAATACTTTGGAATAATACTACAGGGTCAATAAAC	1236
QY	1243	ATAATCACACTCCAATGCAGAAATAAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAANA	1302
DB	1237	AATATCACACTTCAATGCAAAAATAAAAACAAATTATAAACCATGTGGCAGGAAGTAGGAANA	1296
QY	1303	GCAATGTATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTG	1362
DB	1297	GCAATGTATGCCCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTA	1356
QY	1363	CTACTAACAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT	1419
DB	1357	CTATTAAACAAGAGATGGTGTAAAGGACACGGACACGAACGACCCGAGATCTTCAGACCT	1416
QY	1420	GGAGGAGGAGATATAGGGACAATTTGGAGAAGTGAATTATATAAATAATAAGTAGTAAGA	1479
DB	1417	GGAGGAGGAGATATAGGGACAATTTGGAGAAGTGAATTATATAAATAATAAGTAGTAACA	1476
QY	1480	ATTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAAGAACAGTGCACAAAGAGAAAAA	1539
DB	1477	ATTGAACCAATTAGGAGTAGCACCCACCAGGGCAAGAGAAGAGTGGTGCAGAGAGAAAAA	1536
QY	1540	AGAG	1543
DB	1537	AGAG	1540

**RESULT 10**

US-10-375-777-3

03 10 375 777 ; Sequence 3, Application US/10375777

Publication No. US20030147912A1

; FUDIFICATION NO: 092003  
: GENERAL INFORMATION:

GENERAL INFORMATION: APPLICANT: Johnson, Philip R.

AFFILIANT: GUMSON, PHILIP A.  
 TITLE OF INVENTION: Adeno-Associated Virus Materials and

**TITLE OF INVENTION:** Agents for Methods

NUMBER OF SEQUENCES: 3 me

NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:

;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein, Murray & Borup

;  
ADDRESS: MAIRHALL, 0 1001E, GERSCHEIN, MULLA,  
STREET: 6300 Sears Tower 233 S Wacker Drive

STREET: 6300 se  
CITY: Chicago

CITY: Chicago  
STATE: IllinoisSTATE: ILLINOIS  
COUNTRY: USA

```

; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.2.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,777
; FILING DATE: 26-Feb-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20030147912Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
; US-10-375-777-3

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Query Match	52.1%;	Score 1172.4;	DB 15;	Length 2571;
Best Local Similarity	88.2%;	Pred. No. 3.4e-264;		
Matches 1327; Conservative	0;	Mismatches 156;	Indels 21;	Gaps 4;

QY	58	TCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG	117
DB	40	TGGGGATGGGGCAGATGCTCCTTGGGTTAATAATGATCTGTAGTGTACAGAAAAATTG	99
QY	118	TGGGTCACAGTCTATTATATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTTTGT	177
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QY	178	GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGT	237
DB	160	GCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGGCCACACAGCCTGT	219
QY	238	GTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAAC	297
DB	220	GTACCCACAGACCCCAACCCCAAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAAC	279
QY	298	ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA	357
DB	280	ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA	339
QY	358	AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACCTAATTG	417
DB	340	AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACCTGATTG	399
QY	418	-----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG	465
DB	400	AGGAATACTACTAATAACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGGGGAACA	459
QY	466	ATGGAGAAAGGAGAAATAFAAAAAATTGCTCTTTCTATATCAACCAAGCATATAGAAATAAG	525
DB	460	ATAAAGGGAGGAGAAATGAAAAAATCTGCTCTTTTCAATATACCAACAAGCATATAGAGATAAG	519
QY	526	GTAAGAAGAAAGAAATATGCACTTTTAAATAGACTTGTATAGTACCAATAGAAAAATCTAAT	585
DB	520	ATGCAGAAAGAAATATGCACTTCTTTATATAAACTTGTATAGTATCAATAG--ATAATGAT	576



Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTCAC TGATAATGCTAAACCATCATAGTACAT 876  
QY 886 CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCAAACAATAACAAGAAGGTTA 945  
Db 877 CTGAATGAATCTGTACAAATTAATTGTACAAGACCCAACTACAATAAAGAAAAGGATA 936  
QY 946 TCTATAGGACCGAGGAGCAATTTATGCAAGAGAAACAATAATAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACCGAGGAGCAATTTATACAACAACAAAATAATAATAGGAACATAAGACAA 996  
QY 1006 GCACATTGTAACATTAGTAGACCAAAATGGAATAACACTTTACAACAGATAGTTATAAAA 1065  
Db 997 GCACATTGTAACATTAGTAGACCAAAATGGAATGACACTTTAAGACAGATAGTTAGCAA 1056  
QY 1066 TTAAGAGAAAAATTTAGGATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCA 1125  
Db 1057 TTAAGAAGAACAAATTTAAGAAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116  
QY 1126 GAAATTTGAATGCACAGTTTAAATTTGTGGAGGGGAATCTTCTACTGTAATACAGCACAA 1185  
Db 1117 GAAATTTGAATGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176  
QY 1186 CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGACAAATGGCACTGAAGGAATGAC 1242  
Db 1177 CTGTTTAATAGTACTTGGAAATGGTAATAATACTTGGAAATAATACTACAGGGTCAATAAC 1236  
QY 1243 ATAATCACACTCCAATGCAGATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAA 1296  
QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCTCCCATTGAAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTA 1356  
QY 1363 CTACTAACAAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACCGGACACGAAACGACACCGAGATCTTCAGACCT 1416  
QY 1420 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAACA 1476  
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QY 1540 AGAG 1543  
Db 1537 AGAG 1540

RESULT 12  
US-09-966-931-27  
; Sequence 27, Application US/09966931  
; Publication No. US20030064361A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
; STREET: 3 Embarcadero Center  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/966,931  
; FILING DATE: 27-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/492,739  
; FILING DATE: 2000-01-27  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haliday, Emily  
; REGISTRATION NUMBER: 38903  
; REFERENCE/DOCKET NUMBER: 14918-704  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-393-2000  
; TELEFAX: 415-393-2286  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2552 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2552  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-966-931-27  
  
Query Match 52.0%; Score 1171.8; DB 10; Length 2552;  
Best Local Similarity 89.0%; Pred. No. 4.7e-264;  
Matches 1334; Conservative 0; Mismatches 132; Indels 33; Gaps 5;  
  
QY 64 TCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC 123  
Db 46 TGGGCGACCATGCTCCTTGGGATGTTGATGATCTGTAGTCTGCAGAAAAATTGTGGGTC 105  
  
QY 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACACCACACTCTATTTTGTGCATCA 183  
Db 106 ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACACCACACTCTATTTTGTGCATCA 165  
  
QY 184 GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC 243  
Db 166 GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC 225  
  
QY 244 ACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303  
Db 226 ACAGACCCCAACCCACAAGAATAGGATTGGAAATGTAACAGAAAAATTTTAAACATGTGG 285  
  
QY 304 AAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363  
Db 286 AAAAAATAACATGGTAGAACAAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTA 345  
  
QY 364 AAGCCATGTGTAAAAATTAAACCCCACTGTGTGTTACTTTTAAATTGCACATAATTGTAATATC 423  
Db 346 AAGCCATGTGTAAAAATTAAACCCCACTATGTGTTACTTTTAAATTGCACATGATTG----- 399  
  
QY 424 ACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA 483  
Db 400 ---AAAAATGCTACTAATACTACCTAGTAGCAGCTGGGGAAGATGGAGAGAGGAGAGAAATA 456  
  
QY 484 AAAAAATTGCTCTTTCTATATCAACAAGCATAAAGAAATAAGTAAAGTAAAGAAAGAAATATGCA 543  
Db 457 AAAAACTGCTCTTTCAATGTCTACCACAAGTATAAGAGATAAGATGAAGAATGAATATGCA 516  
  
QY 544 CTTTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTA 603  
Db 517 CTTTTTATAAACTTGTAGTAGTACCAATAG---ATAATGATAATACTAGCTATAGGTTG 573  
  
QY 604 ATAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATT 663  
Db 574 ATAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTGTCTTTTGAGCCCAATT 633  
  
QY 664 CCCATACATTATTGTGTCCCCGGCTGGGTTTCCGATGCTAAAGTGTAAACAATAAGACATT 723



Db	634	 CCCATACATTATTTGTGCCCCGGCTGTTTTTGGCATTTCTAAAGTTAGAGATAAAAAGTTC	693
Qy	724	 AATGGATCAGGACCATGTCACAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCA	783
Db	694	 AACGGAACAGGACCATGTACAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCA	753
Qy	784	 GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA	843
Db	754	 GTAGTATCAACTCAACTGCTGTTAAATGGCAGTTTAGCAGAAAGAAAGTAGTAATTAGA	813
Qy	844	 TCTGAAAAATTTTCACAGACAAATGCTAAAAACCATAATAGTACAGTAAATGAATCTGTAGTA	903
Db	814	 TCTGCCAAATTTCTCGGACAAATGCTAAACCATAATAGTACAGCTGAACGAATCTGTAGAA	873
Qy	904	 ATTAATTGTACAAGACCCCAACAACAATACAAGAAAGAGTTATCTATAGGACCAGGGAGA	963
Db	874	 ATTAATTGTACAAGACCCCAACAACAATACAAGAAAGAGTATACATATAGGACCAGGGAGA	933
Qy	964	 GCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGT	1023
Db	934	 GCATTTTATGCAACAGAGAAATAATAGGAGACATAAGACAAGCACATTGTAAACCTTAGT	993
Qy	1024	 AGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTTAGG	1083
Db	994	 AGCACAAATGGAATAATACTTTAAAACAGATAGTTACAAAATTAAGAGAACATTTT---	1050
Qy	1084	 AATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCACAGT	1143
Db	1051	 AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCCAGAAAATTGTAATGCACAGT	1110
Qy	1144	 TTTAATTGTGAGGGGAATTCTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTGG	1203
Db	1111	 TTTAATTGTGAGGGGAATTTTCTACTGTAATACAACACCACCTGTTTAATAGTACTTGG	1170
Qy	1204	 AATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGA-----CATAAATCACA	1251
Db	1171	 AATTATACTTATCTTGAATAATACTGAAGGGTCAAAATGACACTGGAAGAAATATCACA	1230
Qy	1252	 CTCCAATGCAGAAATAAAACAAATTATAAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT	1311
Db	1231	 CTCCAATGCAGAAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTAT	1290
Qy	1312	 GCCCCCTCCCATCAGGACAAATTAGATGTTCTACATAATTTACAGGGCTGCTACTAACA	1371
Db	1291	 GCCCCCTCCCATAAGAGACAAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTAAACA	1350
Qy	1372	 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT	1431
Db	1351	 AGAGATGGTGGTAATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAGAT	1404
Qy	1432	 ATGAGGGACAAATTTGGAGAAAGTGAAATTATATAAATATAAAGTAGTAAGAAATTGAAACCAATA	1491
Db	1405	 ATGAGGGACAAATTTGGAGAAAGTGAAATTATATAAATATAAAGTAGTAAAAATTTGAACCATTA	1464
Qy	1492	 GGAGTAGCACCCACAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAAGAGGGGAGG	1550
Db	1465	 GGAGTAGCACCCACCAAGGCAAAAGAGAAAGAGTAGTGTCAGAGAGAAAAAAGACGAGTGGG	1523

**RESULT 13**

US-10-459-121-27  
; Sequence 27, Application US/10459121  
; Publication No. US20040121317A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; Nakamura, Gerald R.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
; STREET: 3 Embarcadero Center  
; CITY: San Francisco

```
Qy 544 CTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGCTTA 603
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 517 CTTTTTATAAACTTGATGTAGTACCAATAG--ATAATGATAATACTAGCTATAGGTG 573
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy .604 ATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAAGGTATCCTTTTCAGCCAATT 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 574 ATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAAGGTCTCCTTTGAGCCAATT 633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 664 CCATACATTATTGTGTCCTGGCTGGGTTTGCATGCTAAAGTGTAAACAATAAGACATTC 723
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 634 CCATACATTATTGTGCCCCGGCTGGTTTTCGATTCTAAAAGTGTAGAGATAAAAAAGTTC 693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 724 AATGGATCAGGACCATGCACAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCA 783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 694 AACGGAACAGGACCATGTACAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCA 753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 784 GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTAGA 843
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 754 GTAGTATCAACTCAACTGCTGTTAAATGGCAGTTTAGCAGAGAAGATAGTAATTAGA 813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 844 TCTGAAAAATTCACAGACAATGCTAAAAACCATAAATAGTACAGCTAAATGAATCTGTAGTA 903
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 814 TCTGCCAATTTCTCGGACAATGCTAAAAACCATAAATAGTACAGCTGAACGAATCTGTAGAA 873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 904 ATTAATTGTACAAGACCCCAACAATAACAAGAAGGTTATCTATAGGACCAGGAGA 963
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 874 ATTAATTGTACAAGACCCCAACAATAACAAGAAGGTTATACATATAGGACCAGGAGA 933
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 964 GCATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGT 1023
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 934 GCATTTTATGCAACAGGAGAAATAATAGGAGACATAAGACAAGCACATTGTAACCTTAGT 993
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1024 AGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTAGG 1083
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 994 AGCAGAAAATGGAATAATACTTTAAAACAGATAGTTACAAAATTAAGAGAACATTIT--- 1050
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1084 AATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATGTAATGCACAGT 1143
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1051 AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGCCCAAGAAATGTAATGCACAGT 1110
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1144 TTTAATTGTGGAGGGGAATTCCTTACTGTAATACAGCACAACTGTTTAATAGTACTTGG 1203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1111 TTTAATTGTGGAGGGGAATTTTCTACTGTAATACAACCACTGTTTAATAGTACTTGG 1170
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1204 AATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGA-----CATAAATCACA 1251
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1171 AATTATACTTATACTTGGAATAATACTGAAGGGTCAAAATGACACTGGAAGAAATATCACA 1230
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1252 CTCCAAATGCAGAAATAAAACAAATTTATAAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT 1311
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1231 CTCCAAATGCAGAAATAAAACAAATTTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTAT 1290
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1312 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTTAACA 1371
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1291 GCCCTCCCATAGAGGACAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTTAACA 1350
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1431
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1351 AGAGATGGTGGTAATA-----ACAGCCAAACCGAGATCTTCAGACCTGGAGGAGAGAT 1404
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1432 ATGAGGACAAATTGGAGAAAGTGAATTTATAAAATATAAAGTAGTAAGAAATGAACCAATA 1491
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1405 ATGAGGACAAATTGGAGAAAGTGAATTTATAAAATATAAAGTAGTAAGAAATGAACCAATA 1464
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1492 GGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAGAGAAAAAGAGGGGGAGG 1550
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1465 GGAGTAGCACCCACCAGGGCAAGAGAGAGTGTGCAGAGAGAAAAAGAGCAGTGGG 1523
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 14

US-09-966-931-29

; Sequence 29, Application US/09966931

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; Publication No. US20030064361A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: 2000-01-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2573
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-966-931-29
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Query Match 51.9%; Score 1168.6; DB 10; Length 2573;
Best Local Similarity 88.1%; Pred. No. 2.7e-263;
Matches 1331; Conservative 0; Mismatches 144; Indels 36; Gaps 4;

Qy 64 TCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGGTC 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCATCA 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 106 ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAACAACCACTCTATTTTGTGCATCA 165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 166 GATGCTAAAGCATATGATACAGAGATACATAATGTTTGGGCCACACATGCCTGTGTACCC 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 244 ACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGG 303
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 ACAGACCCCAACCCCAAGAGTAGTATTGGAAAATGTGACAGAAAAATTTTAACATGTGG 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 304 AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 AAAAATAACATGGTGGACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAAGTTTA 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 364 AAGCCATGTGTAAAAATTAACCCCACTCTGTGTTACTTTAAATTGCACATAATTGAATATC 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 346 AAGCCATGTGTAAAAATTAACCCCACTCTGTGTTACTTTAAATTGCACATGAT----- 396
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QY	424	ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAGAAAAGGAGAAATA	483
Db	397	CGCGGGAATACTACTAATACCAATAGTAGTAGCAGCGGGAAGAAGCTGGAGAAAAGGAGAAATA	456
QY	484	AAAAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAGGTAAAGAAAAGAAATATGCA	543
Db	457	AAAACTGCTCTTTCAATATCACCAAGCGTGAGAGATAAGATGCAGAAAAGAAACTGCA	516
QY	544	CTTTTAAATAGACTTGATGTAGTACCAATAGA-----AAATACTAAT	585
Db	517	CTTTTAAATAAACTTGATATAGTACCAATAGATGATGATAGGAATAGTACTAGGAAT	576
QY	586	AATACTAAGTATAGTTAATAAGTTGTAACACCTCAGTCATTAACACAGGCCTGTCCAAAG	645
Db	577	AGTACTAACTATAGTTGATAAGTTGTAACACCTCAGTCATTAACACAGGCCTGTCCAAAG	636
QY	646	GTATCCTTTCAGCCAATTCCCATACATTATTGTGTCCCGGCTGGTTTTCGGATGCTAAAG	705
Db	637	GTATCATTTGAGCCAATTCCCATACATTTCGTGACCCCGGCTGGTTTTCGGCTTCTAAAG	696
QY	706	TGTAACAATAAGACATTCAAATGGATCAGGACCATGCACAAATGTGAGCACAGTACAATGT	765
Db	697	TGTAATAATAAGACGTTCAATGGATCAGGACCATGCAAAAATGTGAGCACAGTACAATGT	756
QY	766	ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	825
Db	757	ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	816
QY	826	GAAGACATAGTAATTAGATCTGAAAAATTTACAGACACAATGCTAAAACCATATAATAGTACAG	885
Db	817	GGAGAGGTAGTAATTAGATCTGAAAAATTTACGGAACAATGCTAAAACCATATAATAGTACAG	876
QY	886	CTAAATGGAATCTGTAGTAATTAAATTGTACAAGACCCAAACAATAAGAGAAAGGTTA	945
Db	877	CTGACAGAAACCAAGTAAAAATTAATTGTACAAGACCCAAACAATAAGAGAAAGTATA	936
QY	946	TCATAGGACCCAGGGAGAGCATTTTATGCAAGAGAAACAATAAGGAGATATAAGACAA	1005
Db	937	CCTATAGGACCCAGGGAGAGCATTTTATGCAACAGGAGACATAATAGGAAATATAAGACAA	996
QY	1006	GCACATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAA	1065
Db	997	GCACATTGTAACCTTAGTAGAACAGACTGGAATAACACTTTAGGACAGATAGTTGAAAAA	1056
QY	1066	TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA	1125
Db	1057	TTAAGAGAAACAATTTGGGAATAAAAACAATAATCTTTAATCACTCCTCAGGAGGGACCCA	1116
QY	1126	GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCACAA	1185
Db	1117	GAAATTGTAATGCACAGTTTAAATTGTAGAGGGGAATTTTCTACTGTAATACACACAA	1176
QY	1186	CTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGACAAATG-----GCACCTGAAGGAAAT	1239
Db	1177	TTGTTTGACAGTACTTGGGATAATACTAAAGTGTCAATGGCACTAGCACTGAAGAGAAT	1236
QY	1240	GACATAATCACACTCCAATGCAGAAATAAAACAATTAATAAATATGTGGCAGAAAGTAGGA	1299
Db	1237	AGCACAAATCACACTCCCATGCAGAAATAAGCAAAATGTAAACAATGTGGCAGGAAGTAGGA	1296
QY	1300	AAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATATACAGGG	1359
Db	1297	AAAGCAATGTATGCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAATATATACAGGG	1356
QY	1360	CTGCTACTAACCAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCT	1419
Db	1357	TTGCTATTAACAAGAGATGGAGG--TAGTAACAACAGCATGAATGAGACCTTCAGACCT	1413
QY	1420	GGAGGAGGAGATATGAGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGA	1479
Db	1414	GGAGGAGGAGATATGAGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAA	1473

QY	1480	ATTGAACCAATAGGAGTAGCACCCACCAGGGCAAAGAAGAACACAGTGCACAAGAGAAAAA	1533
Db	1474	ATTGAACCATTAGGAGTAGCACCCACCAGGGCAAAGAAGAGTGTTGTGCAGAGAAAAA	1533
QY	1540	AGAGGGGAGG 1550	
Db	1534	AGAGCAGTGGG 1544	
 RESULT 15 US-10-459-121-29 ; Sequence 29, Application US/10459121 ; Publication No. US20040121317A1 ; GENERAL INFORMATION: ; APPLICANT: Berman, Phillip W. ; Nakamura, Gerald R. ; TITLE OF INVENTION: HIV Envelope Polypeptides ; NUMBER OF SEQUENCES: 33 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP ; STREET: 3 Embarcadero Center ; CITY: San Francisco ; STATE: CA ; COUNTRY: USA ; ZIP: 94111 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette ; COMPUTER: IBM Compatible ; OPERATING SYSTEM: DOS ; SOFTWARE: FastSeq for Windows Version 2.0 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/10/459,121 ; FILING DATE: 10-Jun-2003 ; CLASSIFICATION: <Unknown> ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/09/134,075 ; FILING DATE: <Unknown> ; APPLICATION NUMBER: 08/448,603 ; FILING DATE: <Unknown> ; ATTORNEY/AGENT INFORMATION: ; NAME: Haliday, Emily ; REGISTRATION NUMBER: 38903 ; REFERENCE/DOCKET NUMBER: 14918-704 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 415-393-2000 ; TELEFAX: 415-393-2286 ; TELEX: <Unknown> ; INFORMATION FOR SEQ ID NO: 29: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 2573 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) ; FEATURE: ; NAME/KEY: CDS ; LOCATION: 1..2573 ; SEQUENCE DESCRIPTION: SEQ ID NO: 29:  US-10-459-121-29			
 Query Match            51.9%;    Score 1168.6;    DB 17;    Length 2573; Best Local Similarity    88.1%;    Pred. No. 2.7e-263; Matches 1331;    Conservative         0;    Mismatches 144;    Indels    36;    Gaps         4;			
QY	64	TCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAATTTGTGGGTC	123
Db	46	TGGGGCACCATGCTCCTTGGGATATTGATGATCTGTAGTGTCTGCGGGAAATTTGTGGGTC	105
QY	124	ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACACCACACTCTATTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAACAAACCACACTCTATTTTGTGCATCA	165
QY	184	GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTTGGGCCACACATGCCTGTGTACCC	243



Db	166	 GATGCTAAAGCATATGATACAGAGATACATAAATGTTTGGGCCACACATGCTGTGTACCC	225
Qy	244	ACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG	303
Db	226	ACAGACCCCAACCCACAAGAAGTAGTATTGGAAAAATGTGACAGAAAAATTTTAAACATGTGG	285
Qy	304	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
Db	286	AAAAATAACATGGTGGAAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGTTTA	345
Qy	364	AAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAATATC	423
Db	346	AAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTCACATGAT-----	396
Qy	424	ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA	483
Db	397	GCGGGGAATACTACTAATACCAATAGTAGTAGCAGGGGAAAAGCTGGAGAAAGGAGAAATA	456
Qy	484	AAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTTAAAGAAAGAAATATGCA	543
Db	457	AAAAACTGCTCTTTCAATATCACCACAAGCGTGAGAGATAAGATGCAGAAAGAAACTGCA	516
Qy	544	CTTTTAAATAGACTTGATGTAGTACCAATAGA-----AAATACTAAT	585
Db	517	CTTTTAAATAAAGTTGATATAGTACCAATAGATGATGATAGGAATAGTACTAGGAAT	576
Qy	586	AATACTAAGTATAGGTTAAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAG	645
Db	577	AGTACTAACTATAGGTTGATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAG	636
Qy	646	GTATCCTTTTCAGCCCAATTCCCATACATTATTGTGTCCCGGCTGGTTTGGCATGCTAAAG	705
Db	637	GTATCATTTGAGCCCAATTCCCATACATTTCTGTACCCCGGCTGGTTTGGCTTCTAAAG	696
Qy	706	TGTAACAATAAGACATTCATGGATCAGGACCATGCACAAATGTTCAGCACAGTACAATGT	765
Db	697	TGTAATAATAAGACGTTCAATGGATCAGGACCATGCACAAATGTTCAGCACAGTACAATGT	756
Qy	766	ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA	825
Db	757	ACACATGGAATTAGGCCAGTGTATCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA	816
Qy	826	GAAGACATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAAACCAATAATAGTACAG	885
Db	817	GGAGAGGTAGTAATTAGATCTGAAAAATTTACGHAACAATGCTAAAAACCAATAATAGTACAG	876
Qy	886	CTAAATGAATCTGTAGTAATTAAATTGTACAAGACCCCAACAATAACAAGAAAGGTTA	945
Db	877	CTGACAGAAACCAAGTAATAAATTAAATTGTACAAGACCCCAACAATAACAAGAAAGTATA	936
Qy	946	TCTATAGGACCCAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAA	1005
Db	937	CCTATAGGACCCAGGAGAGCATTTTATGCAACAGGAGACATAATAGGAAATATAAGACAA	996
Qy	1006	GCACATTGTAACATTAGTAGAGCAAAAATGGAATAACACTTTACAACAGATAGTTATAAAA	1065
Db	997	GCACATTGTAACCTTAGTAGAACAGACTGGAATAACACTTTAGGACAGATAGTTGAAAAA	1056
Qy	1066	TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA	1125
Db	1057	TTAAGAGAAACAATTTGGGAATAAAACAATAATCTTTAATCACTCCTCAGGAGGGACCCA	1116
Qy	1126	GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTGTATAACAGACAA	1185
Db	1117	GAAATTTGTAATGCACAGTTTAAATTTGTAGAGGGGAATTTTCTACTGTAATACAACACAA	1176
Qy	1186	CTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGGCAAAATG-----GCACCTGAAGGAAAT	1239
Db	1177	TTGTTTGACAGTACTTGGGATAAATACTAAAGTGTCAAAATGGCACTAGCACTGAAGAGAAT	1236
Qy	1240	GACATAATCACACTCCAATGCAGAAATAAAACAATTTATAAAATATGTGGCAGAAAGTAGGA	1299

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Job time : 790.268 secs



Db 138 TCATAGAAGGCTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197

QY 1650 GAAACGATACAGAGATGCAACACAGGAGANAAGATCCTTATCCTTACTGAACCTGTGAGGA 1709

Db 198 GAAACGATACAGAGATGCAACACAGGAGANAAGATCCTTATCCTTACTGAACCTGTGAGGA 257

QY 1710 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATAATGTTAAAACAAAGAGGAGACGAA 1769

Db 258 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATAATGTTAAAACAAAGAGGAGACGAA 317

QY 1770 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 1829

Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 377

QY 1830 CATAAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1889

Db 378 CATAAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 437

QY 1890 CACCATGAGCAACAACCTTGTTAACCTCGAAAAATGGGAAACAGCTGACCCGTTAAAAGACA 1949

Db 438 CACCATGAGCAACAACCTTGTTAACCTCGAAAAATGGGAAACAGCTGACCCGTTAAAAGACA 497

QY 1950 AGGACTCTATTATATCTATGCCCAAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 2009

Db 498 AGGACTCTATTATATCTATGCCCAAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 557

QY 2010 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 2069

Db 558 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 617

QY 2070 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 2129

Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 677

QY 2130 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 2189

Db 678 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 737

QY 2190 AGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 2235

Db 738 AGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 783

RESULT 2

AY416062

LOCUS

DEFINITION

AY416062

AY416062.1 GI:39772022

GSS.

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 786)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 786)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering

FEATURES

source

them based on alignment.

Location/Qualifiers

1..786

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

<1..>786

/gene="TNFSF5"

/locus\_tag="HCM5765"

ORIGIN

Query Match 28.5%; Score 641.2; DB 9; Length 786;

Best Local Similarity 99.5%; Pred. No. 1.4e-148;

Matches 643; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1590 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1649

Db 138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197

QY 1650 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 1709

Db 198 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGCGAGGA 257

QY 1710 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATAATGTTAAAACAAAGAGGAGACGAA 1769

Db 258 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATAATGTTAAAACAAAGAGGAGACGAA 317

QY 1770 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 1829

Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 377

QY 1830 CATAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1889

Db 378 CATAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 437

QY 1890 CACCATGAGCAACAACCTTGTTAACCTCGAAAAATGGGAAACAGCTGACCCGTTAAAAGACA 1949

Db 438 CACCATGAGCAACAACCTTGTTAACCTCGAAAAATGGGAAACAGCTGACCCGTTAAAAGACA 497

QY 1950 AGGACTCTATTATATCTATGCCCAAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 2009

Db 498 AGGACTCTATTATATCTATGCCCAAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 557

QY 2010 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 2069

Db 558 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 617

QY 2070 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 2129

Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 677

QY 2130 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 2189

Db 678 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 737

QY 2190 AGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 2235

Db 738 AGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 783

RESULT 3

CD638712

LOCUS

DEFINITION

CD638712

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

767 bp mRNA linear EST 17-JUN-2003

AGENCOURT\_14532410 NIH MGC\_191 Homo sapiens cDNA clone

IMAGE:30416146 5', mRNA sequence.

CD638712

CD638712.1 GI:31804800

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 767)



AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM215 row: h column: 11  
High quality sequence stop: 564.  
Location/Qualifiers  
1. .767  
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/clone="IMAGE:30416146"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

FEATURES  
source  
1. .767  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:30416146"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 25.3%; Score 570; DB 6; Length 767;  
Best Local Similarity 97.8%; Pred. No. 7.8e-131;  
Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 2010 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGTAGATTTCGAGAGAATCTTACT 2069  
|||||  
Db 447 AGTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGTAGATTTCGAGAGAATCTTACT 506  
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Qy 2070 CAGAGCTGCAAATACCCACAGTTCGCCCAAACCTTGGGGCAACAATCCATTCACTTGGG 2129  
|||||  
Db 507 CAGAGCTGCAAATACCCACAGTTCGCCCAAACCTTGGGGCAACAATCCATTCACTTGGG 566  
|||||  
Qy 2130 AGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 2189  
|||||  
Db 567 AGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTC-ATGTGACTGATCCNAGCNA 625  
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RESULT 4  
CD521613  
LOCUS CD521613  
DEFINITION AGENCOURT 14356206 NIH\_MGC\_191 Homo sapiens cDNA clone  
IMAGE:30413128 5', mRNA sequence.  
ACCESSION CD521613  
VERSION CD521613.1 GI:31453331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 806)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM207 row: j column: 17  
High quality sequence stop: 466.  
Location/Qualifiers  
1. .806  
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/clone="IMAGE:30413128"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 22.4%; Score 505; DB 6; Length 806;  
Best Local Similarity 96.7%; Pred. No. 1.3e-114;  
Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 1590 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 1649  
|||

Db 232 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 291

QY 1650 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 1709

Db 292 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 351

QY 1710 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1769

Db 352 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 411

QY 1770 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGACATGT 1829

Db 412 GAAAGANAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCANATTCGGGACATGT 471

QY 1830 CATAAGTGAGGCCAGCAGTAATAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1889

Db 472 CATAAGTGAGGCCAGCAGTAATAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 531

QY 1890 CACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 1949

Db 532 CACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 591

QY 1950 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 2009

Db 592 AAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 651

QY 2010 AGCTCCATTATAGCCAGCTCTGCCTTAAAGTCCCCCGTAGATTTCGAGAGAACTTACT 2069

Db 652 AGCTCCATTATAGCCAGCTCTGCCTTAAAGTCCCCCGTAGATTTCGAGAGAACTTACT 711

QY 2070 CAGAGCTGCAAATACCCACAGTTCGGCCGCAAAACCTT-GCGGGCAACAATCCATTCACTGG 2128

Db 712 CAGAGCTGCAAATACCCCCAGTTCGGCCCAACCTTGGCGGGCAAAACATCCCTTCCCTTG 771

QY 2129 GAG 2131

Db 772 GGG 774

RESULT 5

AY416063

LOCUS

DEFINITION

AY416063

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AY416063

Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY416063

AY416063.1 GI:39772023

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 783)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 783)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

1..783

/organism="Mus musculus"

gene

ORIGIN

Query Match 20.0%; Score 450.8; DB 9; Length 783;

Best Local Similarity 82.2%; Pred. No. 4.1e-101;

Matches 531; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

QY 1590 TCCAAGAAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1649

Db 138 TCATAGAAGATTGGATAAAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTTCAT 197

QY 1650 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 1709

Db 198 AAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCCTTGTCTGAACCTGTGAGGA 257

QY 1710 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1769

Db 258 GATGAGAAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTTAAACAAAGAAGA--GAA 314

QY 1770 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGACATGT 1829

Db 315 AAAAAAAAACAGCTTTGAAATGCAAAAGAGGTGATGAGATCCTCAAAATTCGAGCACACGT 374

QY 1830 CATAAGTGAGGCCAGCAGTAATAACAAACATCTGTGTGTACAGTGGGCTGAAAAAGGATACTA 1889

Db 375 TGTAAGCGAAGCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGGATATTA 434

QY 1890 CACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 1949

Db 435 TACCATGAAAGCAACTTGGTAATGCTTGAAAATGGGAAACAGCTGACCGTTAAAAAGAGA 494

QY 1950 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 2009

Db 495 AGGACTCTATTATGTCTACACTCAAGTCACCTTCTGTCTTAATCGGAGCCCTTCGAGTCA 554

QY 2010 AGCTCCATTATAGCCAGCTCTGCCTTAAAGTCCCCCGTAGATTTCGAGAGAACTTACT 2069

Db 555 ACGCCCATTCATCGTCGGCTCTGGCTGAAGCCACGACGTGGATCTGAGAGAACTTACT 614

QY 2070 CAGAGCTGCAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 2129

Db 615 CAAGGCGGCAAAATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACCTTGGG 674

QY 2130 AGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 2189

Db 675 CGGAGTGTTTGAATTACAAGCTGGTGCTTCTGTGTTTGTCAACGTCAGTGAAGCAAGCCA 734

QY 2190 AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 2235

Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAAACTC 780

RESULT 6

CD640741

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD640741

AGENCOURT 14542170 NIH MGC\_191 Homo sapiens cDNA clone IMAGE:30414715 5', mRNA sequence.

CD640741

CD640741.1 GI:31808911

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 702)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM211 row: 1 column: 20  
High quality sequence stop: 571.

## FEATURES

## ORIGIN

Query Match	17.7%;	Score 399.4;	DB 6;	Length 702;
Best Local Similarity	95.9%;	Pred. No. 2.7e-88;		
Matches 421;	Conservative 0;	Mismatches 16;	Indels 2;	Gaps 1;
Qy	1590	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	1649	
Db	208	TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	267	
Qy	1650	GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTTACTCTGAACCTGTGAGGA	1709	
Db	268	GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTTACTCTGAACCTGTGAGGA	327	
Qy	1710	GATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGTTAAACAAAGAGGAGACGAA	1769	
Db	328	GATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGTTAAACAAAGAGGAGACGAA	387	
Qy	1770	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT	1829	
Db	388	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT	447	
Qy	1830	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	1889	
Db	448	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	507	
Qy	1890	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA	1949	
Db	508	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA	567	
Qy	1950	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA	2009	
Db	568	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCATCGGGAAGCTTCGAGTCA	627	
Qy	2010	AGCTCCATTTATAGCCAGC	2028	
Db	628	--GCTCATTTATAGCCAGC	644	

RESULT 7  
 CD642064  
 LOCUS  
 DEFINITION  
 CD642064  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 CD642064  
 AGENCOURT 14538852 NIH\_MGC\_191 Homo sapiens cDNA clone  
 IMAGE:30418744 5', mRNA sequence.  
 CD642064  
 CD642064.1 GI:31811566  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 690)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Daniela S. Gerhard, Ph.D.  
 JOURNAL  
 COMMENT

## FEATURES

## ORIGIN

		Query Match	17.5%;	Score 395.2;	DB 6;	Length 690;
		Best Local Similarity	99.0%;	Pred. No. 2.9e-87;		
		Matches 397;	Conservative	0;	Mismatches 4;	Indels 0;
					Gaps	0;
Qy	1590	TCCAAGAAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT				
Db	213	TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT				
Qy	1650	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA				
Db	273	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA				
Qy	1710	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA				
Db	333	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA				
Qy	1770	GAAGAAAACAGCTTTTGAAATGCAAAAAGGTGATCAGAATCCTCBAATTTGCGGCACATGT				



Db	393	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGT	452
Qy	1830	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	1889
Db	453	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGANAAGGATACTA	512
Qy	1890	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	1949
Db	513	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	572
Qy	1950	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTCCA	1990
Db	573	AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTGTCCA	613
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LOCUS			
DEFINITION			
AGENCOURT 14355767 NIH_MGC_191 Homo sapiens cDNA clone			
IMAGE:30412573 5', mRNA sequence.			
CD520208			
CD520208.1 GI:31451926			
EST.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 796)			
NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Daniela S. Gerhard, Ph.D.			
Office of Cancer Genomics			
National Cancer Institute / NIH			
Bldg. 31 Rm10A07 Bethesda, MD 20892			
Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>			
Tissue Procurement: Narayan Bhat			
cDNA Library Preparation: CLONTECH Laboratories, Inc.			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			
Plate: NDCM206 row: c column: 14			
High quality sequence stop: 541.			
Location/Qualifiers			
1. .796			
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/db_xref="taxon:9606"			
/clone="IMAGE:30412573"			
/tissue_type="Pooled"			
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/clone_lib="NIH_MGC_191"			
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."			
ORIGIN			
Query Match 17.3%; Score 389; DB 6; Length 796;			
Best Local Similarity 98.3%; Pred. No. 1.1e-85;			
Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;			

Qy	1590	TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	1644
Db	205	TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	264
Qy	1650	GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	1709
Db	265	GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	324
Qy	1710	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	1769
Db	325	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	384
Qy	1770	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGT	1829
Db	385	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGT	444
Qy	1830	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	1889
Db	445	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	504
Qy	1890	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	1949
Db	505	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	564
Qy	1950	AGGACTCTATTATATCTATGCCCAAGTCA-CCTTCTGTTCCAATCGGGAA	1998
Db	565	AGGACTCTATTATATCTATGCCCAAGTCA-CCTTCTGTTCCAATCGGGAA	614
RESULT 9			
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LOCUS			
DEFINITION			
CN794193 571 bp mRNA linear EST 26-MAY-2004			
sequence.			
CN794193			
CN794193.1 GI:47690173			
EST.			
Bos taurus (cow)			
Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
1 (bases 1 to 571)			
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and Matukumalli,L.K.			
Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle			
Unpublished (2004)			
Contact: Richard G. Baumann			
Bovine Functional Genomics Lab			
ANRI			
BLDG 162; BARC-EAST, Beltsville, MD 20705, USA			
Tel: 3015048604			
Fax: 3015048744			
Email: rbaumann@anri.barc.usda.gov			
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt ' ', -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 18			
Plate: 50 row: H column: 03			
Seq primer: CCTATTAGGTGACACTATAGAAC			
High quality sequence stop: 571.			
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1. .571			
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/dev_stage="Lactating, Neonatal"			
/lab_host="DH10B Tona"			
/clone_lib="BARC 8BOV"			
FEATURES			
source			









Waldhoferstrasse 98, D-69123 Heidelberg, Germany  
Tel: +49 6221 4038 150  
Fax: +49 6221 4038 290  
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES

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source
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/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
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ORIGIN

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Query Match      6.1%; Score 138.2; DB 7; Length 636;
Best Local Similarity 84.7%; Pred. No. 3.6e-23;
Matches 155; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1578 TGGCGGATCGGATCCAAGAAAGTTGGACAAGATAGAAAGGAATCTTCATGAAGA 1637
Db   ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 TGCTGTATATCTTCACAGAAGATTGGACAAGATAGAAAGGAATCTTCATGAAGA 130

QY 1638 TTTGTATTTCATGAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACT 1697
Db   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
129 TTTGTGTTTCATGAAACCGTTACAGAAATGCAACAAAGGGGAGGGTCCTTGTCTTACT 70

QY 1698 GAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAA 1757
Db   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 GAACTGTGAGGAAATTAAAGCCAATTGGAAGCCTTTCTCAAGGAGATAATGCTAAACAA 10

QY 1758 AGA 1760
Db   ||
9 CGA 7
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Search completed: November 12, 2004, 12:49:29  
Job time : 4947.98 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 6345.94 Seconds  
(without alignments)  
16453.933 Million cell updates/sec

Title: US-09-687-864A-13  
Perfect score: 2208  
Sequence: 1 aagcttgccgccatgctgta.....aactcgagtataatctaga 2208

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1471.4	66.6	10000	14	AF038398	AF038398 Simian-Hu
2	1453.8	65.8	2046	6	CQ753919	CQ753919 Sequence
3	1453.8	65.8	2610	6	CQ753921	CQ753921 Sequence
4	1453.8	65.8	9860	14	AF217181	AF217181 Simian-Hu
5	1453.8	65.8	9860	14	SIU89134	U89134 Simian-Huma
6	1453.8	65.8	10501	6	BD161892	BD161892 Nonhuman
7	1448	65.6	9713	14	HIV1U39362	U39362 Human immun
8	1339.8	60.7	2010	6	CQ753923	CQ753923 Sequence
9	1339.8	60.7	2574	6	CQ753925	CQ753925 Sequence
10	1263.2	57.2	2553	14	AY247221	AY247221 HIV-1 iso
11	1242.6	56.3	2568	14	AY426111	AY426111 HIV-1 clo
12	1241	56.2	2568	14	AY426112	AY426112 HIV-1 clo
13	1239.4	56.1	2568	14	AY426110	AY426110 HIV-1 clo
14	1237.8	56.1	2568	14	AY426113	AY426113 HIV-1 clo
15	1237.8	56.1	2568	14	AY426115	AY426115 HIV-1 clo
16	1237.8	56.1	2568	14	AY426117	AY426117 HIV-1 clo
17	1237.8	56.1	2568	14	AY426114	AY426114 HIV-1 clo
18	1236.2	56.0	2568	14	AY426116	AY426116 HIV-1 clo
19	1236.2	56.0	2568	14	AY426116	AY426116 HIV-1 clo

20	1227.4	55.6	3061	14	HIVENVBA1A	M63929 Human immun
21	1225.8	55.5	3807	6	AR034235	AR034235 Sequence
22	1225.8	55.5	3807	6	I12144	I12144 Sequence 5
23	1225.8	55.5	3807	6	I28919	I28919 Sequence 5
24	1225.8	55.5	3808	14	HIVBAL1A	M68893 Human immun
25	1224.6	55.5	2559	14	AY669732	AY669732 HIV-1 iso
26	1223.8	55.4	2547	14	AY426125	AY426125 HIV-1 iso
27	1223.8	55.4	2547	14	AY426127	AY426127 HIV-1 clo
28	1222.2	55.4	2544	14	AY669726	AY669726 HIV-1 iso
29	1222.2	55.4	2547	14	AY426126	AY426126 HIV-1 clo
30	1222.2	55.4	9540	14	HIVJRC5F	M38429 Human immun
31	1221.2	55.3	2568	14	AY247225	AY247225 HIV-1 iso
32	1219	55.2	3211	14	HIVU45960	U45960 Human immun
33	1209.4	54.8	2552	6	I05789	I05789 Sequence 8
34	1208.6	54.7	2559	14	AF025750	AF025750 HIV-1 iso
35	1206.8	54.7	2577	14	AF025763	AF025763 HIV-1 iso
36	1201.2	54.4	3600	14	HIVBRVA	M21098 Human immun
37	1199.2	54.3	8896	14	HIVU63632	U63632 HIV-1 isola
38	1197	54.2	1512	6	AX153805	AX153805 Sequence
39	1197	54.2	1512	6	BD017695	BD017695 Assay met
40	1196	54.2	2565	14	AF025754	AF025754 HIV-1 iso
41	1195.6	54.1	2559	14	HIV1U36877	U36877 Human immun
42	1195.4	54.1	2553	14	HIV1MB314	Y13719 Human immun
43	1195.4	54.1	2571	14	HIVENVVB	L08656 Human immun
44	1195.4	54.1	9074	14	HIVU43096	U43096 Human immun
45	1195	54.1	2559	14	AY247220	AY247220 HIV-1 iso

ALIGNMENTS

RESULT 1	AF038398	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome.	10000 bp	DNA	linear	VRL 02-FEB-1998
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ACCESSION	AF038398	AF038398.1	GI:2828036				
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LOCUS			
DEFINITION Sequence 24 from Patent WO2004001051.			
ACCESSION CQ753919			
VERSION CQ753919.1 GI:44845220			
KEYWORDS			
SOURCE Human immunodeficiency virus 1 (HIV-1)			
ORGANISM Human immunodeficiency virus 1			
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate			
lentivirus group.			
REFERENCE			
AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.			
TITLE Recombinant measles viruses expressing epitopes of antigens of rna			
viruses - use for the preparation of vaccine compositions			
JOURNAL Patent: WO 2004001051-A 24 31-DEC-2003;			
INSTITUT PASTEUR (FR)			
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RESULT 3

CQ753921

LOCUS CQ753921 2610 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 26 from Patent WO2004001051.

ACCESSION CQ753921

VERSION CQ753921.1 GI:44845221

KEYWORDS .

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1

AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.

TITLE Recombinant measles viruses expressing epitopes of antigens of rna viruses - use for the preparation of vaccine compositions

JOURNAL Patent: WO 2004001051-A 26 31-DEC-2003;

INSTITUT PASTEUR (FR)

FEATURES Location/Qualifiers

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TITLE Comparative genetic analysis of simian/human immunodeficiency viruses (SHIVs) with pathogenic property  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 9860)  
AUTHORS Sakai,K., Shinohara,K., Takahashi,E. and Honda,M.  
TITLE Direct Submission  
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Characterization of molecularly cloned simian-human  
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J. Virol. 71 (6), 4218-4225 (1997)  
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Query Match 65.8%; Score 1453.8; DB 14; Length 9860;  
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QY	472	AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG	531
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QY	1432	ATGAGGGACAATTTGGAGAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA	1491
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RESULT 6

BD161892	BD161892	10501 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	Nonhuman primate model of acquired immunodeficiency syndrome.				
DEFINITION	BD161892				
ACCESSION	BD161892.1	GI:27867650			
VERSION	JP 2002159296-A/1.				
KEYWORDS	Simian-Human immunodeficiency virus				
SOURCE	Simian-Human immunodeficiency virus				
ORGANISM	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate				
	lentivirus group.				
REFERENCE	1 (bases 1 to 10501)				
AUTHORS	Shinohara,K., Sakai,K. and Honda,M.				
TITLE	Nonhuman primate model of acquired immunodeficiency syndrome				
JOURNAL	Patent: JP 2002159296-A 1 04-JUN-2002;				
	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE				
	ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH				
COMMENT	OS Simian-human immunodeficiency virus				
	PN JP 2002159296-A/1				
	PD 04-JUN-2002				
	PF 27-NOV-2000 JP 2000360274				
	PI KATSUAKI SHINOHARA,KOJI SAKAI,MITSUO HONDA				





Db 8152 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA 8211

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Qy 1552 AGAAG 1556

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RESULT 7

HIV1U39362

LOCUS

DEFINITION Human immunodeficiency virus type 1 proviral DNA, gag, pol, vif, vpr, vpu, env, tat, rev and nef genes, complete cds.

ACCESSION U39362 M96155

VERSION U39362.2 GI:9409797

KEYWORDS

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

1 (bases 1 to 5029)

Collman,R.G. and Yoon,H.L.

Unpublished

2 (bases 5030 to 9713)

Kim,F.M., Kolson,D.L., Balliet,J.W., Srinivasan,A. and Collman,R.G.

V3-independent determinants of macrophage tropism in a primary human immunodeficiency virus type 1 isolate

J. Virol. 69 (3), 1755-1761 (1995)

95156606

7853514

3 (bases 1 to 9713)

Collman,R., Balliet,J.W., Gregory,S.A., Friedman,H., Kolson,D.L., Nathanson,N. and Srinivasan,A.

An infectious molecular clone of an unusual macrophage-tropic and highly cytopathic strain of human immunodeficiency virus type 1

J. Virol. 66 (12), 7517-7521 (1992)

93059708

1433527

Describes the isolation of the full-length clone and virus strain 89.6

4 (bases 1 to 9713)

Collman,R.G.

Direct Submission

Submitted (24-OCT-1995) Ronald G. Collman, Pulmonary & Critical Care Division, University of Pennsylvania, 522 Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA

5 (bases 1 to 9713)

Collman,R.G.

Direct Submission

Submitted (24-JUL-2000) Ronald G. Collman, Pulmonary & Critical Care Division, University of Pennsylvania, 522 Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA

Sequence updated by submitter

On Jul 24, 2000 this sequence version replaced gi:1055029.

Location/Qualifiers

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ACCESSION			
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VERSION			
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KEYWORDS			
Human immunodeficiency virus 1 (HIV-1)			
SOURCE			
Human immunodeficiency virus 1			
ORGANISM			
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate			
lentivirus group.			
REFERENCE			
1			
AUTHORS			
Tangy,F., Lorin,C., Mollet,L. and Delebeque,F.			
TITLE			
Recombinant measles viruses expressing epitopes of antigens of rna			
viruses - use for the preparation of vaccine compositions			
JOURNAL			
Patent: WO 2004001051-A 28 31-DEC-2003;			
INSTITUT PASTEUR (FR)			
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Db	217	GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGTAGTTTGGGAAATGTGACAGAAAAT	276
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Qy	592	AAGTATAGGTTAATAAGTTGTAAACACCTCAGTCAATTACACAGGCCCTGTCCAAAGGTATCC	651
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ORGANISM	Human immunodeficiency virus 1		
REFERENCE	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate		
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AUTHORS	1		
	Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.		
TITLE	Recombinant measles viruses expressing epitopes of antigens of rna		
	viruses - use for the preparation of vaccine compositions		
JOURNAL	Patent: WO 2004001051-A 30 31-DEC-2003;		
	INSTITUT PASTEUR (FR)		
FEATURES	Location/Qualifiers		
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Query Match			
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Matches 1417; Conservative 0; Mismatches 52; Indels 36; Gaps 1;			
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Db	37	TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	96
QY	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA	171
Db	97	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA	156
QY	172	TTTTGTGTCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
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QY	952	GGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACACAGCACAT	1011
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Db	1081	GTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAAATACAGCACAACTGTTT	1140
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ACCESSION AY426111  
VERSION AY426111.1 GI:37962967  
KEYWORDS .  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.  
REFERENCE 1 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching  
JOURNAL J. Virol. 78 (14), 7565-7574 (2004)  
PUBMED 15220431  
REFERENCE 2 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Direct Submission  
JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA  
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Query Match 56.3%; Score 1242.6; DB 14; Length 2568;  
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RESULT 12  
AY426112 2568 bp DNA linear VRL 28-JUN-2004  
LOCUS HIV-1 clone BaL-1A isolate BaL from USA envelope glycoprotein (env)  
DEFINITION gene, complete cds.  
ACCESSION AY426112  
VERSION AY426112.1 GI:37962969  
KEYWORDS Human immunodeficiency virus 1 (HIV-1)  
SOURCE Human immunodeficiency virus 1  
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
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Coreceptor Switching  
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PUBMED 15220431  
REFERENCE 2 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research  
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA  
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Query Match 56.2%; Score 1241; DB 14; Length 2568;  
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REFERENCE	1 (bases 1 to 2568)				
AUTHORS	Pastore,C., Ramos,A. and Mosier,D.E.				
TITLE	Intrinsic Obstacles to Human Immunodeficiency Virus Type 1				
JOURNAL	J. Virol. 78 (14), 7565-7574 (2004)				
PUBMED	15220431				
REFERENCE	2 (bases 1 to 2568)				
AUTHORS	Pastore,C., Ramos,A. and Mosier,D.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research				
FEATURES	Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA				
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VERSION AY426110.1 GI:37962965  
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ORGANISM Human immunodeficiency virus 1  
REFERENCE 1 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1  
JOURNAL Coreceptor Switching  
PUBMED J. Virol. 78 (14), 7565-7574 (2004)  
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REFERENCE 2 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Direct Submission  
JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research  
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA  
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LOCUS	AY426113	HIV-1 clone Bal-1B isolate Bal from USA	env		
DEFINITION	AY426113	gene, complete cds.			
ACCESSION	AY426113				
VERSION	AY426113.1	GI:37962971			
KEYWORDS					
SOURCE		Human immunodeficiency virus 1 (HIV-1)			
ORGANISM		Human immunodeficiency virus 1			
REFERENCE		Viruses; Retrovirus; Retroviridae; Lentivirus; Primate			
AUTHORS		lenti virus group.			
TITLE		1 (bases 1 to 2568)			
JOURNAL		Pastore, C., Ramos, A. and Mosier, D.E.			
PUBMED		Intrinsic Obstacles to Human Immunodeficiency Virus Type 1			
REFERENCE		Coreceptor Switching			
AUTHORS		J. Virol. 78 (14), 7565-7574 (2004)			
TITLE		15220431			
JOURNAL		2 (bases 1 to 2568)			
PUBMED		Pastore, C., Ramos, A. and Mosier, D.E.			
REFERENCE		Direct Submission			
AUTHORS		Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research			
TITLE		Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA			
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ORIGIN										
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Best Local Similarity 89.7%; Pred. No. 1.8e-251;										
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Job time : 6350.94 secs

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QY	1366	CTAAACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGA	1425
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 15:28:44 ; Search time 724.277 Seconds  
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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
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10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2208	100.0	2209	4 AAF82929	Aaf82929 HIV-1 gp1
2	2152.8	97.5	2252	4 AAF82928	Aaf82928 HIV-1 gp1
3	1866	84.5	2070	4 AAF82930	Aaf82930 HIV-1 gp1
4	1838	83.2	2028	4 AAF82931	Aaf82931 HIV-1 gp1
5	1453.8	65.8	2046	12 ACA63265	ACA63265 HIV-1 imm
6	1453.8	65.8	2610	12 ACA63266	ACA63266 HIV-1 imm
7	1448	65.6	2051	10 AAL56171	Aal56171 HIV trunc
8	1448	65.6	2562	10 AAL56170	Aal56170 Human imm
9	1339.8	60.7	2010	12 ACA63267	ACA63267 HIV-1 imm
10	1339.8	60.7	2574	12 ACA63268	ACA63268 HIV-1 imm
11	1225.8	55.5	3806	2 AAX04767	Aax04767 Env gene
12	1225.8	55.5	3807	2 AAT58551	Aat58551 Human Imm
13	1222.2	55.4	9540	12 ADO52562	Ado52562 Human imm
14	1222.2	55.4	9540	12 ADP20074	Adp20074 Human imm
15	1219	55.2	3807	2 AAQ14753	Aaq14753 HIV-1 BA-
16	1207.8	54.7	2553	1 AAN80949	Aan80949 HIV prote
17	1199.2	54.3	2612	12 ADJ92821	Adj92821 Human imm
18	1199.2	54.3	8896	12 ADP20082	Adp20082 Human imm
19	1197	54.2	1512	5 AAF87100	Aaf87100 HIV-1 gp1
20	1179.8	53.4	1422	12 ADP74731	Adp74731 HIV-1 iso
21	1174.2	53.2	3808	2 AAV58244	Aav58244 Insert re

C	22	1174.2	53.2	3808	2	AAV60252	Aav60252 Insert re
	23	1173	53.1	2553	2	AAQ76018	Aaq76018 DNA encod
	24	1172.2	53.1	2571	2	AAT09010	Aat09010 HIV-1 str
	25	1172.2	53.1	2571	2	AAZ08741	Aaz08741 HIV-1 MN
	26	1172.2	53.1	2571	3	AAA93973	Aaa93973 Human imm
	27	1172.2	53.1	2571	4	AAC86877	Aac86877 Nucleotid
	28	1172.2	53.1	2571	5	AAH43700	Aah43700 Wild type
	29	1172.2	53.1	2571	8	ABX14499	Abx14499 Human imm
	30	1172.2	53.1	2571	9	ADA50072	Ada50072 Human imm
	31	1172.2	53.1	2571	10	AD81077	Ad81077 HIV-1 (MN
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C	33	1172.2	53.1	6474	2	AAQ40300	Aaq40300 Sequence
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ALIGNMENTS

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XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
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DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
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OS Human immunodeficiency virus 1.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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XX  
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XX  
PF 13-OCT-2000; 2000WO-US028414.  
XX  
PR 14-OCT-1999; 99US-0159690P.  
XX  
PA (LEDB/) LEDBETTER J A.

PA (HAYD/) HAYDEN-LEDBETTER M S.  
XX Ledbetter JA, Hayden-Ledbetter MS;  
PI  
DR WPI; 2001-281790/29.  
XX P-PSDB; AAB62334.  
PT DNA vaccine for improving antigen-specific humoral and cellular immune  
PT responses, comprising one or more antigens linked to a domain that binds  
PT at least one receptor.  
XX  
PS Example 1; Fig 3A; 55pp; English.  
XX  
CC The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC long form extracellular domain fusion protein linked by a ProAspPro  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;  
  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Qy 61 GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGAGTACCTTCTGTTTGGATCTCG 120  
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Db 121 GTCACAGTCTATTATGGGTACTGTGTGGAGATATTGATGATCTGAGTACCTTCTGTTTGGCA 180  
  
Qy 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA 240  
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Db 541 GCACTTTTTAATAGACTTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGG 600  
  
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Db 601 TTAATAAAGTTGTAAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTTATCCTTTTCAGCCA 660  
  
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Qy 1621 AGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAAAGCCAG 1680  
Db 1621 AGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAAAGCCAG 1680  
  
Qy 1681 TTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAAGAAACACAGC 1740  
Db 1681 TTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAAGAAACACAGC 1740  
  
Qy 1741 TTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCACATGTCTAAGTGAGGCC 1800

Db 1741 TTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGCACATGTCATAAGTGAGGCC 1800

Qy 1801 AGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1860

Db 1801 AGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1860

Qy 1861 AACTTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT 1920

Db 1861 AACTTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT 1920

Qy 1921 ATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1980

Db 1921 ATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1980

Qy 1981 GCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAAT 2040

Db 1981 GCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAAT 2040

Qy 2041 ACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 2100

Db 2041 ACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 2100

Qy 2101 TTGCAACCAAGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCAAAGTGAGCCATGGC 2160

Db 2101 TTGCAACCAAGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCAAAGTGAGCCATGGC 2160

Qy 2161 ACTGGCTTCAGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2208

Db 2161 ACTGGCTTCAGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2208

RESULT 2

AAF82928

ID AAF82928 standard; cDNA; 2252 BP.

XX

AC AAF82928;

XX

DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX

DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.

XX

KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine; acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX

OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX

FH Key

FT CDS

FT 13..2252

FT Location/Qualifiers

FT sig\_peptide

FT 13..72

FT /tag= a

FT /tag= b

FT /note= "synthetic secretory signal peptide"

FT 73..1542

FT /tag= c

FT /note= "HIV-1 gp120 domain coding sequence"

FT misc\_feature

FT 1543..1593

FT /tag= d

FT /note= "[Gly4Ser]3 linker coding sequence"

FT misc\_feature

FT 1594..2252

FT /tag= e

FT /note= "human CD154 long form extracellular domain coding sequence"

XX

PN WO200126608-A2.

XX

PD 19-APR-2001.

XX

PF 13-OCT-2000; 2000WO-US028414.

XX

PR 14-OCT-1999; 99US-0159690P.

XX (LEDB/) LEDBETTER J A.

PA (HAYD/) HAYDEN-LEDBETTER M S.

XX

PI Ledbetter JA, Hayden-Ledbetter MS;

XX

DR WPI; 2001-281790/29.

DR P-PSDB; AAB62333.

XX

PT DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PT

XX

PS Example 1; Fig 3A; 55pp; English.

XX

CC The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3 linker. (Updated on 11-SEP-2003 to standardise OS field)

CC

XX

SQ Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;

Query Match 97.5%; Score 2152.8; DB 4; Length 2252;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 2206; Conservative 0; Mismatches 2; Indels 42; Gaps 1;

Qy 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Db

Qy 61 GCTTCGAGATCCATGCTCCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Qy 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCCTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCCTCTATTTTGTGCA 180

Qy 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCTGTGTA 240

Db 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCTGTGTA 240

Qy 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAACATG 300

Qy 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Qy 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTTGAAT 420

Db 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTTGAAT 420

Qy 421 ATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Db 421 ATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Qy 481 ATAAAAAATGCTCTTTCTATATCACCAAGCATACCAAGGTAAGGTAAGAAAGAAATAT 540

Db 481 ATAAAAAATGCTCTTTCTATATCACCAAGCATACCAAGGTAAGGTAAGAAAGAAATAT 540

Qy 541 GCACCTTTTAATAGACTTTGATGTAGTACCAATAGAAAAFACTAATACTAAGTATAGG 600

Db 541 GCACCTTTTAATAGACTTTGATGTAGTACCAATAGAAAAFACTAATACTAAGTATAGG 600

Qy 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660

Db 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660



QY	661	ATTCCCATACATTATTGTGTC	CGGCTGGGTTTGGCATGCTAAAGTGTAAACAATAAGACA	720	QY	1699	GATATAATGTTAAACAAAGAGGAGACGAAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGT	1758	
Db	661				Db	1741			
QY	721	TTCAATGGATCAGGACCATG	CACAAAATGT	CAGCACAGTACAAATGTACACATGGAATTAGG	780	QY	1759	GATCAGAAATCCTCAAATTCGGGCACATGTCAATAAGTGAGGCCAGCAGTAAAAACAACATCT	1818
Db	721				Db	1801			
QY	781	CCAGTGGTGTCAACTCAACTG	CTGTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT	840	QY	1819	GTGTTACAGTGGGCTGAAAAAGGATACACCATGAGCAACAACCTTGGTAAACCTGGAA	1878	
Db	781				Db	1861	GTGTTACAGTGGGCTGAAAAAGGATACACCATGAGCAACAACCTTGGTAAACCTGGAA	1920	
QY	841	AGATCTGAAAAATTTTCACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA	900	QY	1879	AATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC	1938		
Db	841				Db	1921	AATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC	1980	
QY	901	GTAATTAAATTGTACAAGACCCAAACAACAATACAAGAAAGGTTTATCTATAGGACCAGGG	960	QY	1939	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATAGCCAGCCTCTGCCTAAAAG	1998		
Db	901				Db	1981	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCAATTTATAGCCAGCCTCTGCCTAAAAG	2040	
QY	961	AGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACAATTGTAACATT	1020	QY	1999	TCCCCCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAA	2058		
Db	961				Db	2041	TCCCCCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAA	2100	
QY	1021	AGTACAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAAATTAAGAGAAAAATTT	1080	QY	2059	CCTTGGGGGCAACAATCCATTCACCTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCG	2118		
Db	1021				Db	2101	CCTTGGGGGCAACAATCCATTCACCTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCG	2160	
QY	1081	AGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAATGCAC	1140	QY	2119	GTGTTTGTCAATGTGACTGATCCAAGCCAAAGTGAGCCATGGCATTGCAGTCCCTTT	2178		
Db	1081				Db	2161	GTGTTTGTCAATGTGACTGATCCAAGCCAAAGTGAGCCATGGCATTGCAGTCCCTTT	2220	
QY	1141	AGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACT	1200	QY	2179	GGCTTACTCAAACTCGAGTGATAATCTAGA	2208		
Db	1141				Db	2221	GGCTTACTCAAACTCGAGTGATAATCTAGA	2250	
QY	1201	TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC	1260	RESULT 3					
Db	1201				AAF82930				
QY	1261	AGAAATAAAACAAATTATAAATAATGTGGCAGAAAAGTAGGAAAAAGCAATGTATGCCCTCCC	1320	ID	AAF82930	standard; cDNA; 2070 BP.			
Db	1261				XX	AAF82930;			
QY	1321	ATCAGAGCAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGA	1380	XX	11-SEP-2003 (revised)				
Db	1321				DT	29-JUN-2001 (first entry)			
QY	1381	GGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGAGAGGAGGATATGAGGGAC	1440	XX	HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.				
Db	1381				DE	Antigen; receptor; humoral; cellular; immune response; DNA vaccine;			
QY	1441	AATTGGAGAAAGTGAAATTATATAAATATAAAGTAGTAAGAAATTGAAACCAATAGGAGTAGCA	1500	KW	acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;				
Db	1441				KW	HIV-1; gp120; human; CD154; fusion protein; ss.			
QY	1501	CCCACAGGGCAAAGAGAAAGAACAGTGCAAAAGAGAAAAA	1540	XX	Human immunodeficiency virus 1.				
Db	1501				OS	Homo sapiens.			
QY	1541	-----GACCGGATCCAAAGAGGTTGGACAAGATAGAAAGGAGGCGGTTTCAGGA	1560	XX	Location/Qualifiers				
Db	1561	GGTGGAGGTTCTGGAGGTGGCGGATCGGATCCAAGAAAGTTGGACAAGATAGAAAGATGAA	1620	FT	13. .2070				
QY	1579	AGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA	1638	FT	/*tag= a				
Db	1621	AGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAGAGATGCAACACAGGAGAA	1680	FT	13. .72				
QY	1639	AGATCCCTTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAG	1698	FT	/*tag= b				
Db	1681	AGATCCCTTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAG	1740	FT	/note= "synthetic secretory signal peptide"				
				FT	73. .1542				
				FT	/*tag= c				
				FT	/note= "HIV-1 gp120 domain coding sequence"				
				FT	1543. .1593				
				FT	/*tag= d				
				FT	/note= "[Gly4Ser]3 linker coding sequence"				
				FT	1594. .2070				
				FT	/*tag= e				
				FT	/note= "human CD154 short form extracellular domain coding sequence"				
				XX					
				PN	WO200126608-A2.				

XX 19-APR-2001.  
XX 13-OCT-2000; 2000WO-US028414.  
XX 14-OCT-1999; 99US-0159690P.  
XX (LEDB/) LEDBETTER J A.  
PA (HAYD/) HAYDEN-LEDBETTER M S.  
PA  
XX Ledbetter JA, Hayden-Ledbetter MS;  
PI  
XX WPI; 2001-281790/29.  
DR P-PSDB; AAB62335.  
DR  
XX  
PT DNA vaccine for improving antigen-specific humoral and cellular immune  
PT responses, comprising one or more antigens linked to a domain that binds  
PT at least one receptor.  
XX  
PS Example 1; Fig 3B; 55pp; English.  
PS  
CC The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC short form extracellular domain fusion protein linked by (Gly4Ser)3  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;  
Query Match 84.5%; Score 1866; DB 4; Length 2070;  
Best Local Similarity 92.2%; Pred. No. 0;  
Matches 2035; Conservative 0; Mismatches 35; Indels 138; Gaps 1;  
QY 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60  
DB 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60  
QY 61 GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTGCTACAGAAAAATTGGG 120  
DB 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTCTGCTACAGAAAAATTGGG 120  
QY 121 GTCACAGTCTATTATGGGGTACCTGTGTGAGGAGTACATAATGTTTGGGCCACACATGCTTGTGCA 180  
DB 121 GTCACAGTCTATTATGGGGTACCTGTGTGAGGAGTACATAATGTTTGGGCCACACATGCTTGTGCA 180  
QY 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTTGTGCA 240  
DB 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTTGTGCA 240  
QY 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTACAGAAAAATTTTAAACATG 300  
DB 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTACAGAAAAATTTTAAACATG 300  
QY 301 TGGAAAAATAACATGGTAGATCAGATGAGGATATAATCAGTTTATGGGATGAAAGC 360  
DB 301 TGGAAAAATAACATGGTAGATCAGATGAGGATATAATCAGTTTATGGGATGAAAGC 360  
QY 361 CTAAAGCCATGTGTAAATTAACCCACTCTGTGTTACTTTTAAATGCACTAATTTGAAT 420  
DB 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTTAAATGCACTAATTTGAAT 420  
QY 421 ATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAA 480  
DB 421 ATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAA 480  
QY 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATTAAGGTAAAGAAATAT 540  
DB 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATTAAGGTAAAGAAATAT 540  
QY 541 GCACTTTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGG 600

DB 541 GCACTTTTTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGG 600  
QY 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660  
DB 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660  
QY 661 ATTCCCATACATTATTGTGCCCGCTGGGTTTGCATGCTAAAGTGTAAACAATAAGACA 720  
DB 661 ATTCCCATACATTATTGTGCCCGCTGGGTTTGCATGCTAAAGTGTAAACAATAAGACA 720  
QY 721 TTCAATGGATCAGGACCATGCACAAAATGTCAGCACAGTACAAATGTACACATGGAATTAGG 780  
DB 721 TTCAATGGATCAGGACCATGCACAAAATGTCAGCACAGTACAAATGTACACATGGAATTAGG 780  
QY 781 CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840  
DB 781 CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840  
QY 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA 900  
DB 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA 900  
QY 901 GTAATTAATTGTACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACCAGGG 960  
DB 901 GTAATTAATTGTACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACCAGGG 960  
QY 961 AGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATT 1020  
DB 961 AGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATT 1020  
QY 1021 AGTAGAGCAAAAATGGAATTAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTT 1080  
DB 1021 AGTAGAGCAAAAATGGAATTAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTT 1080  
QY 1081 AGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCAC 1140  
DB 1081 AGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCAC 1140  
QY 1141 AGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCACAACTGTTTAATAGTACT 1200  
DB 1141 AGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCACAACTGTTTAATAGTACT 1200  
QY 1201 TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGCACATAATCACACTCCAATGC 1260  
DB 1201 TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGCACATAATCACACTCCAATGC 1260  
QY 1261 AGAATAAAACAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320  
DB 1261 AGAATAAAACAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320  
QY 1321 ATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAGAGATGGA 1380  
DB 1321 ATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAGAGATGGA 1380  
QY 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGAGAGGAGGAGATATGAGGGAC 1440  
DB 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGAGAGGAGGAGATATGAGGGAC 1440  
QY 1441 AATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500  
DB 1441 AATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500  
QY 1501 CCCACCAGGGCAAAGAGAAAGACAGTGCAAAAGAGAAAAAAGAGGG----- 1545  
DB 1501 CCCACCAGGGCAAAGAGAAAGACAGTGCAAAAGAGAAAAAAGAGGG----- 1545  
QY 1561 GACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCATGAAAAACGATACAG 1620  
DB 1546 ----- 1546  
QY 1621 AGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAGCCAG 1680

Db 1546 ----- 1545

Qy 1681 TTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGAGACGAAGAAACACAGC 1740

Db 1546 ---GGAGGCGGTTTCAGGAGGTGGAGGTTCTGGAGGTGGCGGATCGGATCCAGAAAACAGC 1602

Qy 1741 TTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGTCTATAAGTGAGGCC 1800

Db 1603 TTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGTCTATAAGTGAGGCC 1662

Qy 1801 AGCAGTAAACAACATCTGTGTGTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1860

Db 1663 AGCAGTAAACAACATCTGTGTGTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1722

Qy 1861 AACTTGGTAACCCCTGGAAAAATCGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT 1920

Db 1723 AACTTGGTAACCCCTGGAAAAATCGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT 1782

Qy 1921 ATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1980

Db 1783 ATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1842

Qy 1981 GCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAAT 2040

Db 1843 GCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAAT 1902

Qy 2041 ACCCAGAGTTCGGCCAAACCTTGGCGGGCAACAATCCATTCACCTTGGGAGGAGTATTGAA 2100

Db 1903 ACCCAGAGTTCGGCCAAACCTTGGCGGGCAACAATCCATTCACCTTGGGAGGAGTATTGAA 1962

Qy 2101 TTGCAACCCAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAAAGCCAAGTGAGCCATGGC 2160

Db 1963 TTGCAACCCAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAAAGCCAAGTGAGCCATGGC 2022

Qy 2161 ACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAATCTAGA 2208

Db 2023 ACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAATCTAGA 2070

RESULT 4

AAF82931

ID AAF82931 standard; cDNA; 2028 BP.

XX AC AAF82931;

DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.

XX KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 13..2028

FT /\*tag= a

FT sig\_peptide 13..72

FT /\*tag= b

FT /note= "synthetic secretory signal peptide"

FT misc\_feature 73..1542

FT /\*tag= c

FT /note= "HIV-1 gp120 domain coding sequence"

FT misc\_feature 1543..1551

FT /\*tag= d

FT /note= "ProAspPro linker coding sequence"

FT misc\_feature 1552..2028

FT /\*tag= e

FT /note= "human CD154 short form extracellular domain coding sequence"

XX WO200126608-A2.

PN 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028414.

PF 14-OCT-1999; 99US-0159690P.

XX (LEDB/) LEDBETTER J A.

PA (HAYD/) HAYDEN-LEDBETTER M S.

XX Ledbetter JA, Hayden-Ledbetter MS;

XX WPI; 2001-281790/29.

DR P-PSDB; AAB62336.

XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PT Example 1; Fig 3B; 55pp; English.

XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be use against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;

SQ Query Match 83.2%; Score 1838; DB 4; Length 2028;

Best Local Similarity 91.8%; Pred. No. 0;

Matches 2028; Conservative 0; Mismatches 0; Indels 180; Gaps 1;

Qy 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Db 1 AAGCTTGCCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Qy 61 GCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Qy 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA 180

Qy 181 TCAGATGCTAAAGCCATATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGTGTA 240

Db 181 TCAGATGCTAAAGCCATATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGTGTA 240

Qy 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

Qy 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Qy 361 CTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCACATAATTGAA 420

Db 361 CTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCACATAATTGAA 420

Qy 421 ATCAGTAAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Db 421 ATCAGTAAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Qy 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAAATAAGGTAAGAAAGAAATAT 540

Db 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAAATAAGGTAAGAAAGAAATAT 540











XX OS Human immunodeficiency virus.  
XX FH Key Location/Qualifiers  
XX PF CDS 1..2001  
FT /\*tag= a  
FT /product= "truncated gp 160"  
XX PN WO2003077838-A2.  
XX PD 25-SEP-2003..  
XX PF 05-MAR-2002; 2002WO-US007144.  
XX PR 05-MAR-2002; 2002WO-US007144.  
XX PA (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.  
XX PI Dimitrov DS, Chow Y, Phogat SK, Broder CC;  
XX WPI; 2003-779074/73.  
DR P-PSDB; ABU64219.  
XX New HIV antigenic composition comprising an HIV envelope glycoprotein 160 having a glycoprotein 120 subunit covalently linked to a glycoprotein 41 subunit useful for protecting a human from HIV infection.  
XX Disclosure; Page 62-63; 65pp; English.  
CC The present invention relates to an HIV antigenic composition, comprising an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41 subunit, where the carboxy-terminal end of gp120 is covalently linked through a peptide linker of at least 5 amino acids, to the amino-terminal end of gp41. The HIV antigenic composition is useful for protecting a human from HIV infection, potentially in the form of a vaccine. The present sequence is the HIV truncated gp160 coding sequence  
SQ Sequence 2051 BP; 749 A; 333 C; 467 G; 502 T; 0 U; 0 Other;  
Query Match 65.6%; Score 1448; DB 10; Length 2051;  
Best Local Similarity 98.8%; Pred. No. 1.6e-285;  
Matches 1470; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGCT---ACAGAAAAATTGTGGGTACAGT 128  
DB 51 CTTGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAAAAAAGAAAAACGTGGGTCAAA 110  
QY 129 CTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGC 188  
DB 111 CTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGC 170  
QY 189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGA 248  
DB 171 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGA 230  
QY 249 CCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAA 308  
DB 231 CCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAA 290  
QY 309 TAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCC 368  
DB 291 TAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCC 350  
QY 369 ATGTCTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACCTAAATTTGAATATCACTAA 428  
DB 351 ATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACCTAAATTTGAATATCACTAA 410  
QY 429 GAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAATAAAAAA 488  
DB 411 GAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAATAAAAAA 470  
QY 489 TTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAGAAAGAAATATGCACITTT 548  
|||||

DB 471 TTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGAAATAATGCACTTTT 530  
QY 549 TAAATAGACTTGAITAGTACCAATAGAAAAATACTTAATAATACTAAGTATAGGTTAATAAG 608  
DB 531 TAAATAGACTTGAITAGTACCAATAGAAAAATACTTAATAATACTAAGTATAGGTTAATAAG 590  
QY 609 TTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAATTCCCAT 668  
DB 591 TTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAATTCCCAT 650  
QY 669 ACATTATTGTGTCCTCCGCTGGGTTTGGCGATGCTAAAGTGTAAACAATAAGACATTCAATGG 728  
DB 651 ACATTATTGTGTCCTCCGCTGGGTTTGGCGATGCTAAAGTGTAAACAATAAGACATTCAATGG 710  
QY 729 ATCAGGACCATTGCACAAATGTCAGCACAGTACAATGTACACATGGAAATTAGGCCAGTGGT 788  
DB 711 ATCAGGACCATTGCACAAATGTCAGCACAGTACAATGTACACATGGAAATTAGGCCAGTGGT 770  
QY 789 GTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGA 848  
DB 771 GTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGA 830  
QY 849 AAATTTTCACAGACAATGCTAAAAACCATAAATAGTACAGCTAAATGAATCTGTAGTAATAA 908  
DB 831 AAATTTTCACAGACAATGCTAAAAACCATAAATAGTACAGCTAAATGAATCTGTAGTAATAA 890  
QY 909 TTGTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCAT 968  
DB 891 TTGTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCAT 950  
QY 969 TTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTTAACATTAGTAGAGC 1028  
DB 951 TTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTTAACATTAGTAGAGC 1010  
QY 1029 AAAATGGAATAACACTTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATAA 1088  
DB 1011 AAAATGGAATAACACTTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATAA 1070  
QY 1089 AACAAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTTGTAATGCACAGTTTAA 1148  
DB 1071 AACAAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTTGTAATGCACAGTTTAA 1130  
QY 1149 TTGTGGAGGGGAATTCCTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTGGAAATGT 1208  
DB 1131 TTGTGGAGGGGAATTTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTGGAAATGT 1190  
QY 1209 TACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1268  
DB 1191 TACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1250  
QY 1269 ACAAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1328  
DB 1251 ACAAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1310  
QY 1329 ACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG 1388  
DB 1311 ACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG 1370  
QY 1389 TACTGAGACTGAGACTGAGACTTTCAGACCTTCAGAGGAGGAGATATGAGGGACAAATTTGGAG 1448  
DB 1371 TACTGAGACTGAGACTGAGACTTTCAGACCTTCAGAGGAGGAGATATGAGGGACAAATTTGGAG 1430  
QY 1449 AAGTGAATTATATAAATATAAAGTAGTAAGAAATGAAACCAATAGGAGTAGCACCCACCAG 1508  
DB 1431 AAGTGAATTATATAAATATAAAGTAGTAAGAAATGAAACCAATAGGAGTAGCACCCACCAG 1490  
QY 1509 GGCAAGAGAGAAACAGTGCNAAAGAGAAAAAGACCCGGATCCCAAGAAG 1556  
DB 1491 GGCAAGAGAGAAACAGTGCNAAAGAGAAAAAGAGCAGTGGGAATAGG 1538  
RESULT 8  
AAL56170



Db 1431 AAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAG 1490  
QY 1509 GGCAAGAGAGAACAGTGCRAAGAGAGAAAAAGACCCGGATCCAAGAAG 1556  
Db 1491 GGCAAGAGAGAGAACAGTGCRAAGAGAGAAAAAGAGCAGTGCGGAATAGG 1538  
RESULT 9  
ACA63267  
ID ACA63267 standard; DNA; 2010 BP.  
XX  
AC ACA63267;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE HIV-1 immunogenic sequence #3.  
XX  
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
KW immunogenic; virucide; ds.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO2004001051-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 20-JUN-2003; 2003WO-EP007146.  
XX  
PR 20-JUN-2002; 2002EP-00291550.  
XX  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
PI Tangy F, Lorin C, Mollet L, Delebecque F;  
XX WPI; 2004-082508/08.  
DR  
XX  
PT New recombinant mononegavirales measles virus expressing a heterologous  
PT amino acid, useful for preparing immunogenic or vaccine composition for  
PT the prophylaxis or treatment of measles.  
XX  
PS Disclosure; Fig 16E; Opp; English.  
XX  
CC The present invention relates to a recombinant mononegavirales measles  
CC virus expressing a heterologous amino acid, which is capable of eliciting  
CC a humoral and/or cellular immune response against the heterologous amino  
CC acid sequence including in individuals having pre-existing measles virus  
CC immunity. The recombinant virus is useful for preparing immunogenic or  
CC vaccine composition for the prophylaxis or treatment of measles. The  
CC present sequence is a HIV immunogenic sequence shown in the  
CC exemplification of the invention  
XX  
SQ Sequence 2010 BP; 720 A; 326 C; 469 G; 495 T; 0 U; 0 Other;  
Query Match 60.7%; Score 1339.8; DB 12; Length 2010;  
Best Local Similarity 94.2%; Pred. No. 1.8e-263;  
Matches 1417; Conservative 0; Mismatches 52; Indels 36; Gaps 1;  
QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111  
Db 37 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 96  
QY 112 AAATTGTGGGTACACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171  
Db 97 AAATTGTGGGTACACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 156  
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231  
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216  
QY 232 GCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAATGTGACAGAAAAT 291

Db 217 GCCTGTGTACCCACAGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAT 276  
QY 292 TTTAACATGTGGAAAAATAAACATGGTAGATCAGATGAGATGAGGATATAATCAGTTTATGG 351  
Db 277 TTTAACATGTGGAAAAATAAACATGGTAGATCAGATGAGATGAGGATATAATCAGTTTATGG 336  
QY 352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCAC 411  
Db 337 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCAC 396  
QY 412 AATTGGAATATCACTAAGAATACTACTAATCTCCTAGTAGCAGCTGGGGAATGATGGAG 471  
Db 397 AATTGGAATATCACTAAGAATACTACTAATCTCCTAGTAGCAGCTGGGGAATGATGGAG 456  
QY 472 AAAGGAGAAAATAAAAAATTGCTCTTTCTATATCACACAAGCATAAGAAAATAAGGTAAAG 531  
Db 457 GAAGGAGAAAATAAAAAATTGCTCTTTCTATATCACACAAGCATAAGAAAATAAGGTAAAG 516  
QY 532 AAAGGAATATGCACCTTTTAAATAGACTTGTGATGTAGTACCAATAGAAAAATACATAATACT 591  
Db 517 AAAGGAATATGCACCTTTTAAATAGACTTGTGATGTAGTACCAATAGAAAAATACATAATACT 576  
QY 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTATACACAGGCCTGTCCAAAGGTATCC 651  
Db 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTATACACAGGCCTGTCCAAAGGTATCC 636  
QY 652 TTTTCAGCCAATTCCCATACATATTATTGTGTCCCCTGCGGTTTTCGGATGCTAAAGGTAAAC 711  
Db 637 TTTTCAGCCAATTCCCATACATATTATTGTGTCCCCTGCGGTTTTCGGATGCTAAAGGTAAAC 696  
QY 712 AATAAGACATTTCAATGGATCAGGACCATGCACAATGTTCAGCACAGTACAATGTACACAT 771  
Db 697 AATAAGACATTTCAATGGATCAGGACCATGCACAATGTTCAGCACAGTACAATGTACACAT 756  
QY 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGCTTTAAATGGCAGTCTAGCAGAGAAAGAC 831  
Db 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGCTTTAAATGGCAGTCTAGCAGAGAAAGAC 816  
QY 832 ATAGTAATTAGATCTGAAAAATTTTACAGACAAATGCTFAAAACCATAATAATAGTACAGCTAAAT 891  
Db 817 ATAGTAATTAGATCTGAAGATTTTACAGACAAATGTTTAAAAACCATAATAATAGTACAGCTAAAT 876  
QY 892 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTTATCTATA 951  
Db 877 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATGC----- 917  
QY 952 GGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACAT 1011  
Db 918 -----TGCAGAATTGGATAAATGGCAAGTGTGCAAGACACAAGCACAT 960  
QY 1012 TGTAAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGA 1071  
Db 961 TGTAAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGA 1020  
QY 1072 GAAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 1131  
Db 1021 GAAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 1080  
QY 1132 GTPAATGCACAGTTTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTT 1191  
Db 1081 GTPAATGCACAGTTTTTAAATTGTGGAGGGGAATTTTCTACTGTAATACAGCACAACTGTTT 1140  
QY 1192 AATAGTACTTTGGAATGTTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1251  
Db 1141 AATAGTACTTTGGAATGTTTCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1200  
QY 1252 CTCCAATGCAGAATAAAACAATTTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT 1311  
Db 1201 CTCCAATGCAGAATAAAACAATTTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT 1260  
QY 1312 GCCCTCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA 1371  
Db 1261 GCCCTCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA 1320



QY	1372	AGAGATGGAGGTAATAGTACTGAGACCTGAGACTGAGATCTTCAGACCCTGGAGGAGGAGAT	1431
Dd	1321	AGAGATGGAGGTAATAGTACTGAGACCTGAGACTGAGATCTTCAGACCCTGGAGGAGGAGAT	1380
QY	1432	ATGAGGGACAATTGGAGBACTGAATTATATAAATATAAAAGTAGTAAGAATTGAACCAATA	1491
Dd	1381	ATGAGGGACAATTGGAGBACTGAATTATATAAATATAAAAGTAGTAAGAATTGAACCAATA	1440
QY	1492	GGAGTAGCACCCACCAGGC AAAGAGAAAGAACAGTGCAAAGAGAAAAAGACCCGATCCA	1551
Dd	1441	GGAGTAGCACCCACCAGGC AAAGAGAAAGAACAGTGCAAAGAGAAAAAGAGCAGTGGGA	1500
QY	1552	AGAAG	1556
Dd	1501	ATAGG	1505

**RESULT 10**

ACA63268

ID ACA63268 standard; DNA; 2574 BP.

XX

AC ACA63268;

XX

DT 22-APR-2004 (first entry)

XX

DE HIV-1 immunogenic sequence #4.



KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
KW immunogenic; virucide; ds.



OS Human imm

XX

PN WO2004001

[illegible]

PD 31-DEC-20

XX DE 20-11M-20

FF  
YY  
20-JUN-20

XX  
PP  
20-11N-20

FR 20-JUN-2002; 2002EF-00291330:  
XX

PA (TNSP) T

PA (CNRS) CENT NAT RECH SCI.  
PA (CNRS) INST PASIEUR:XX  
(CNRS / C

PI Tangv F. Lorin C. M

xx  
xx

DR WPI; 2004

[illegible]

**PT** New recom

PT amino acid, useful f

PT the proph

XX  
PS Disclosure; Fig 16G; Opp; English.

2000

cc The prese

CC virus expressing a heterologous am

CC a humoral

acid sequence including in individuals having pre-existing measles virus immunity. The recombinant virus is useful for preparing immunogenic or vaccine composition for the prophylaxis or treatment of measles. The present sequence is a HIV immunogenic sequence shown in the exemplification of the invention

XX

SQ Sequence 2574 BP; 864 A; 440 C; 637 G; 633 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 94.2%; Pred. No. 1.8e-263;

Matches 1417; Conservative 0; Mismatches 52;

52 Qy

QY	112	AAATTGTGGGTACAGTCTATTATAGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA	171
Db	97	AAATTGTGGGTACAGTCTATTATAGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA	156
QY	172	TTTGTGTCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	157	TTTGTGTCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	216
QY	232	GCCTGTGTACCCACAGACCCCAACCCACCAAGAGTAGTATTGGGAAATGTGACAGAAAAT	291
Db	217	GCCTGTGTACCCACAGACCCCAACCCACCAAGAGTAGTATTGGGAAATGTGACAGAAAAT	276
QY	292	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
Db	277	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	336
QY	352	GATGAAAGCCTAAAGCCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTTAAATTGCAC	411
Db	337	GATGAAAGCCTAAAGCCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTTAAATTGCAC	396
QY	412	AATTTGAATATCACTAAGAAATACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAG	471
Db	397	AATTTGAATATCACTAAGAAATACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAG	456
QY	472	AAAGGAGAAATAAAAAAATTGCTCTTTCTATATACCAACCAAGCATAAGAAATAAGGTAAAG	531
Db	457	GAAGGAGAAATAAAAAAATTGCTCTTTCTATATACCAACCAAGCATAAGAAATAAGGTAAAG	516
QY	532	AAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT	591
Db	517	AAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT	576
QY	592	AAGTATAGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC	651
Db	577	AAGTATAGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC	636
QY	652	TTTCAGCCAAATCCCACATATTATTGTGTCGGCTGGGTTTGGATGCTAAAGTGTAAAC	711
Db	637	TTTCAGCCAAATCCCACATATTATTGTGTCGGCTGGGTTTGGATGCTAAAGTGTAAAC	696
QY	712	AATAAGACATTCAAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAAATGTACACAT	771
Db	697	AATAAGACATTCAAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAAATGTACACAT	756
QY	772	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAGAC	831
Db	757	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAGAC	816
QY	832	ATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAAACCATAATAGTACAGCTAAAT	891
Db	817	ATAGTAATTAGATCTGAAAGATTTACAGACAAATGTTAAAAACCATAATAGTACAGCTAAAT	876
QY	892	GAATCTGTAGTAATTAATTGTACAAGACCCCAACAAATACAAAGAAAGGTTATCTATA	951
Db	877	GAATCTGTAGTAATTAATTGTACAAGACCCCAACAAATACAAAGAAAGGTTATCTATA	917
QY	952	GGACCAGGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACAT	1011
Db	918	-----TGCAGAAATTGGATAAATGGCAAGTGCTGCAAGACAAGCACAT	960
QY	1012	TGTAACATTTAGTAGAGCAAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAAATTAAGA	1071
Db	961	TGTAACATTTAGTAGAGCAAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAAATTAAGA	1020
QY	1072	GA AAAATTTAGGAATAAAA CAATAGCCTTTAAATCAATCCTCAGGAGGGGACCCAGAAAAT	1131
Db	1021	GA AAAATTTAGGAATAAAA CAATAGCCTTTAAATCAATCCTCAGGAGGGGACCCAGAAAAT	1080
QY	1132	GTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACCTGTTT	1191
Db	1081	GTAATGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATACAGCACAACCTGTTT	1140
QY	1192	AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCAGCTGAAGGAAATGACATAATCACA	1251

Db 1141 AATAGTACTTGAATGTTGCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1200  
QY 1252 CTCCAATGCAGATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT 1311  
Db 1201 CTCCAATGCAGATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT 1260  
QY 1312 GCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATATTACAGGGCTGCTACTAACA 1371  
Db 1261 GCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATATTACAGGGCTGCTACTAACA 1320  
QY 1372 ACAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCCTGGAGGAGGAGAT 1431  
Db 1321 ACAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCCTGGAGGAGGAGAT 1380  
QY 1432 ATGAGGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAATTGBACCAATA 1491  
Db 1381 ATGAGGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAATTGBACCAATA 1440  
QY 1492 GGAGTAGCACCCACCAGGGCAAGAGAAACAGTGCAAAGAGAAAAAGACCGGATCCA 1551  
Db 1441 GGAGTAGCACCCACCAGGGCAAGAGAAACAGTGCAAAGAGAAAAAGACGAGTGGGA 1500  
QY 1552 AGAAG 1556  
Db 1501 ATAGG 1505

RESULT 11  
AAX04767  
ID AAX04767 standard; DNA; 3806 BP.  
XX  
AC AAX04767;  
XX  
DT 17-OCT-2003 (revised)  
DT 09-APR-1999 (first entry)  
XX  
DE Env gene of the BA-L strain of Human immunodeficiency virus type 1.  
XX  
KW HIV-1; HIV-1 strain BA-L; env protein; vaccine; immunotherapy;  
KW HIV infection; immunogen; HIV-1 diagnosis; ds.  
XX  
OS Human immunodeficiency virus 1.  
XX  
FH Location/Qualifiers  
FT 648..3214  
FT /\*tag= a  
FT /product= "env\_protein"  
FT /transl\_except= (pos: 678..678, aa: Gln)  
XX  
PN US5869313-A.  
XX  
PD 09-FEB-1999.  
XX  
PF 14-MAY-1996; 96US-00647714.  
XX  
PR 17-OCT-1990; 90US-00599491.  
PR 25-FEB-1993; 93US-00022835.  
PR 15-FEB-1995; 95US-00388809.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Gallo RC, Franchini G, Reitz MS, Lori FC, Popovic M, Gartner S;  
PI Markham PD;  
XX  
DR WPI; 1999-152779/13.  
DR p-PSDB; AAW88113.  
XX  
PT DNA encoding env protein of the human immune deficiency virus isolate BA-  
PT L - useful for producing protein for use in vaccines, as assay reagent  
PT and to generate antibodies.  
XX  
PS Claim 2; Fig 8A-H; 87pp; English.

XX The present sequence encodes the envelope protein of the BA-L (ATCC  
CC 40890) strain of Human immunodeficiency virus type 1 (HIV-1) strain MN-  
CC ST1. BA-L is more typical of United States isolates of HIV-1 than  
CC previously known strains. Recombinant, complete env protein of the BA-L  
CC strain is used as a vaccine component and for immunotherapy of existing  
CC HIV infections, to detect HIV-specific antibodies, e.g. in donated blood,  
CC and as an immunogen to raise specific antibodies, for HIV-1 diagnosis.  
CC (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 3806 BP; 1306 A; 662 C; 937 G; 901 T; 0 U; 0 Other;  
Query Match 55.5%; Score 1225.8; DB 2; Length 3806;  
Best Local Similarity 89.9%; Pred. No. 3.4e-240;  
Matches 1340; Conservative 0; Mismatches 142; Indels 9; Gaps 2;  
QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTACAGTCTA 131  
Db 700 CATGCTCCTTGGGATATTGATGATCTGTAATGCTGAAGAAAAATTGTGGGTACAGTCTA 759  
QY 132 TTATGGGGTACCTGTGTGGAGAGAAAGCAACCACACTCTATTTTGTGTCATCAGATGCTAA 191  
Db 760 TTATGGGGTACCTGTGTGGAGAGAAAGCAACCACACTCTATTTTGTGTCATCAGATGCTAA 819  
QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251  
Db 820 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 879  
QY 252 CAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGRAAAAATAA 311  
Db 880 CAACCCACAAGAAGTAGAATTGAAAAATGTGACAGAAAAATTTTAACATGTGGAATAATAA 939  
QY 312 CATGGTAGATCAGATGTCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATG 371  
Db 940 CATGGTAGAACAAATGTCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATG 999  
QY 372 TGTAAAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGA-----ATATCAC 425  
Db 1000 TGTAAAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAGGAATGCTACTAA 1059  
QY 426 TAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAATAAA 485  
Db 1060 TGGGAATGACACTAATACCACCTAGTAGCAGGGGAAATGGTGGGGGAGGAGAAATGAA 1119  
QY 486 AAATTGCTCTTTCTATATACCAACAGCATAAGAAATAAGGTAAAGAAAGATATGCACT 545  
Db 1120 AAATTGCTCTTTCAATATACCAACAACATAAGAGGTAAGGTGCAGAAAGATATGCACT 1179  
QY 546 TTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAAT 605  
Db 1180 TTTTATAAACTTGATATAGCACCATAATAGATAATAATAGTAATAATAGATATAGGTTGAT 1239  
QY 606 AAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCAAAGGTATCCTTTACGCCAATTCC 665  
Db 1240 AAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCAAAGGTATCCTTTGAGCCAAATCC 1299  
QY 666 CATACATTTATGTGTCGGCTGGGTTTTCGATGCTFAAAGTGTAAACAATAAGACATTCAA 725  
Db 1300 CATACATTTATGTGCCCCGGCTGGTTTTCGATTCCTAAAGTGTAAAGATAAGAAAGTTCAA 1359  
QY 726 TGGATCAGGACCATGCACAAATGTGAGCAGCATACATGTACACATGGAATTAGGCCAGT 785  
Db 1360 TGGAAAAGGACCATGTACAAATGTGAGCAGCATACATGTACACATGGAATTAGGCCAGT 1419  
QY 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGCTCTAGCAGAAAGACATAGTAATTAGATC 845  
Db 1420 AGTATCAACTCAACTGCTGTTAAATGGCAGCTCTAGCAGAAAGAGGAGGTAGTAATTAGATC 1479  
QY 846 TGAAAAATTTACAGACAAATGCTAAAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAAT 905  
Db 1480 CGCCAAATTTGCGGACAAATGCTAAAAGTCAATAATAGTACAGCTGAATGAATCTGTAGAAAT 1539  
QY 906 TAAATTGTACAAGAGACCCCAACAATAACAAGAAAGGTTATCTATAGGACCAGGGAGAGC 965

Db 1540 TAAATTGTACAAGACCCCAACAATAACAAGAAAAAGTATACATATAGGACCGCAGAGC 1599  
QY 966 ATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAGCACATTGTAAACATTAGTAG 1025  
Db 1600 ATTTTATACAACAGGAGAAATAATAGGAGATATAAGACAGCACATTGTAAACCTTAGTAG 1659  
QY 1026 AGCAAAATGGAATAACACTTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAA 1085  
Db 1660 AGCAAAATGGAATGACACTTTTAAATAAGATAGTTTATAAAATTAAGAGAACAATTTGGAA 1719  
QY 1086 TAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTGTAATGCACAGTTT 1145  
Db 1720 TAAACAATAGTCTTTAAGCACTCTCAGGAGGGGCCCAAGAAATTGTGACGCACAGTTT 1779  
QY 1146 TAATTGTGGAGGGAATTCCTTACTGTAAATACAGCACAACTGTTTAATAGTACTTGGAA 1205  
Db 1780 TAATTGTGGAGGGAATTTTCTACTGTAAATTCACACAACTGTTTAATAGTACTTGGAA 1839  
QY 1206 TGTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAT 1265  
Db 1840 TGTACTGAAGAGTCAAATAACACTGTAGAAAAATAACAATAACACACTCCCATGCAGAAT 1899  
QY 1266 AAAACAAATTATAATATGTGCAGAAAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCAC 1325  
Db 1900 AAAACAAATTATAACATGTGCAGGAAGTAGGAAGAGCAATGTATGCCCTCCCATCAG 1959  
QY 1326 AGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAA 1385  
Db 1960 AGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--- 2016  
QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 1445  
Db 2017 TCCTGAGGACAACAAGACCGAGTCTTCAGACCTGGAGGAGGAGATATGAGGGATAATTG 2076  
QY 1446 GAGAAGTGAATTATATAATAATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCAC 1505  
Db 2077 GAGAAGTGAATTATATAATAATAAAGTAGTAAGAAAAATTGAACCATTAGGAGTAGCACCCAC 2136  
QY 1506 CAGGGCAAAGAGAGACAGTGCACAAAGAGAAAAAGACCGGATCCAAGAAG 1556  
Db 2137 CAAGGCAAAGAGAGAGTGGTGCGAGAGAGAAAAAGAGCAAGTGGGAATAGG 2187

RESULT 12  
AAT58551  
ID AAT58551 standard; cDNA; 3807 BP.

AC AAT58551;  
XX AAT58551;  
DT 17-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 25-MAR-1997 (first entry)  
XX Human Immunodeficiency Virus-1 strain BA-L env gene.  
DE Acquired immune deficiency syndrome; AIDS; envelope protein; env gene;  
XX vaccine; ds.  
XX Human immunodeficiency virus 1; (strain BA-L).  
OS Key Location/Qualifiers  
XX 648. .3215  
FH CDS /\*tag= a  
FT /product= "envelope\_protein"  
XX  
PN US5576000-A.  
XX  
PD 19-NOV-1996.  
XX  
PF 15-FEB-1995; 95US-00388809.  
XX  
PR 17-OCT-1990; 90US-00599491.

PR 25-FEB-1993; 93US-00022835.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA Gallo RC, Franchini G, Lori FC, Popovic M, Reitz MS, Gartner S;  
PI Markham PD;  
XX WPI; 1997-011206/01.  
DR P-PSDB; AAW11581.  
XX New isolated envelope protein of HIV-1 strain BA-L and recombinant  
PT equivalents - useful as immunogens for vaccines and antibody prodn.,  
PT typical of US clinical isolates.  
XX Example; Fig 8; 86pp; English.  
PS A HindIII fragment of unintegrated viral DNA representing the BA-L genome  
XX was cloned into lambda phage Charon 28 DNA from total DNA of peripheral  
CC blood lymphocytes infected with and producing HIV-1(BA-L). A positive  
CC clone was selected by hybridisation using a HIV-1 env probe. This clone,  
CC designated BA-L1, was found to contain the entire gene for the envelope  
CC protein on a 2.8 kb HindIII-XbaI fragment and a 0.4 kb EcoRI-HindIII  
CC fragment. When cloned together these fragments comprise the env gene, as  
CC well as the coding regions for rev and the rev-responsive element of env,  
CC both necessary for efficient expression in eukaryotic cells. The claimed  
CC recombinantly produced envelope protein can be used as an immunogen for  
CC raising antibodies against HIV. (Updated on 25-MAR-2003 to correct PF  
CC field.) (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 3807 BP; 1307 A; 662 C; 937 G; 901 T; 0 U; 0 Other;  
Query Match 55.5%; Score 1225.8; DB 2; Length 3807;  
Best Local Similarity 89.9%; Pred. No. 3.4e-240;  
Matches 1340; Conservative 0; Mismatches 142; Indels 9; Gaps 2;  
QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTGTGGTCACAGTCTA 131  
Db 701 CATGCTCCTTGGGATATTGATGATCTGTAAATGCTGAAGAAAAAATTGTGGTCACAGTCTA 760  
QY 132 TTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAA 191  
Db 761 TTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACTCTATTTTGTGCATCAGATCCTAA 820  
QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251  
Db 821 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 880  
QY 252 CAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAATAA 311  
Db 881 CAACCCACAAGAGTAGAATTGAAAAATGTGACAGAAAAATTTTAACATGTGGAAAAATAA 940  
QY 312 CATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATG 371  
Db 941 CATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATG 1000  
QY 372 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCACATAATTGA-----ATATCAC 425  
Db 1001 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCACATAATTGAGGAATGCTACTAA 1060  
QY 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAA 485  
Db 1061 TGGGAATGACACTAATACCACCTAGTAGTAGCAGGGGAATGTTGGGGGGAGGAGAAATGAA 1120  
QY 486 AAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAGAAAGAATATGCACT 545  
Db 1121 AAATTGCTCTTTCAATATCACCACAACATAGAGGTAAAGTGCAGAAAGAATATGCACT 1180  
QY 546 TTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAAT 605  
Db 1181 TTTTATAAACTTGATATAGCACCATAATAGATAATAATAATAGTAATAATAGATATAGGTTGAT 1240  
QY 606 AAGTTGTAACACCTCAGTCATTACACAGGCCTGTCAAAGGTTATCCTTTTCAGCCAAFTCC 665



Db 1241 AAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAGCCAATTCC 1300

QY 666 CATACATTATTGTGCCGGCTGGGTTTGCATGCTAAAAGTGTAAACAATAAGACATTCAA 725

Db 1301 CATACATTATTGTGCCCGGCTGGTTTTCGATTCTAAAAGTGTAAAGATAGAAGTTCAA 1360

QY 726 TGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT 785

Db 1361 TGGAAAAGGACCATGTACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT 1420

QY 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATC 845

Db 1421 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATC 1480

QY 846 TGA AAAATTTACAGACAAATGCTAAAAACCATAAATAGTACAGCTAAATGAATCTGTAGTAAT 905

Db 1481 CGCCAATTTTCGGGACAAATGCTAAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540

QY 906 TAAATGTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCGAGAGAGC 965

Db 1541 TAAATGTACAAGACCCCAACAATAACAAGAAAAGTATACATATAGGACCGAGAGC 1600

QY 966 ATTTTATGCAAGAAGAACATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGTAG 1025

Db 1601 ATTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAAACCTTAGTAG 1660

QY 1026 AGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAATTTAGGAA 1085

Db 1661 AGCAAAATGGAATGACACTTTAAATAAGATAGTTATAAAATTAAGAGAACAAATTTGGAA 1720

QY 1086 TAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCAGTTT 1145

Db 1721 TAAAACAATAGTCTTTAAGCACTCCTCAGGAGGGGACCCAGAAAATTGTACGCACAGTTT 1780

QY 1146 TAAATGTGAGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAATAGTACTTGGAA 1205

Db 1781 TAAATGTGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAATAGTACTTGGAA 1840

QY 1206 TGTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAT 1265

Db 1841 TGTACTGAAGAGTCAATTAACACTGTAGAAAATAACAAATCACACTCCCCATGCAGAAT 1900

QY 1266 AAAACAAATTATAAATATGTGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1325

Db 1901 AAAACAAATTATAACATGTGGCAGGAAGTAGGAAGAGCAATGTATGCCCTCCCATCAG 1960

QY 1326 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGTAA 1385

Db 1961 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG- -- 2017

QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGAGGAGATATGAGGGACAATTG 1445

Db 2018 TCCTGAGGACAACAAGACCGAGGTCTTCAGACCTGGAGAGGAGATATGAGGGATAATTG 2077

QY 1446 GAGAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCAC 1505

Db 2078 GAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCAC 2137

QY 1506 CAGGGCAAAGAGAACAAGTGCAAAAGAGAAAAAAGACCGGATCCAAGAAG 1556

Db 2138 CAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGG 2188

RESULT 13

ADO52562

ID ADO52562 standard; DNA; 9540 BP.

XX

AC ADO52562;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human immunodeficiency virus 1 parent JRCSEF DNA.

XX

KW Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy; vaccine; ds.

XW

XX Human immunodeficiency virus 1.

OS

XX

PN US2004101823-A1.

XX

PD 27-MAY-2004.

XX

PF 19-DEC-2002; 2002US-00325468.

XX

PR 21-DEC-2001; 2001US-0343524P.

XX

PA (MAXY-) MAXYGEN INC.

XX

PI Soong NW, Pekrun K, Shibata R;

XX

DR WPI; 2004-399670/37.

DR

XX GENBANK; M38429.

PT New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a composition for treating or preventing infection caused by HIV-1.

XX

PS Disclosure; SEQ ID NO 46; 310pp; English.

XX

CC The present invention relates to human immunodeficiency virus 1 (HIV-1) viral variants and nucleic acids and polypeptides thereof having improved replication properties for development of suitable animal models for the study of HIV-1 pathogenesis. The invention is useful for treating and preventing HIV-1 infection. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the invention.

CC

XX

SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 55.4%; Score 1222.2; DB 12; Length 9540;

Best Local Similarity 90.0%; Pred. No. 2.1e-239;

Matches 1337; Conservative 0; Mismatches 133; Indels 15; Gaps 2;

QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAAATTTGGGTACAGTCTA 131

Db 6289 CTTGCTCCTTGGGACATTAATGATCTGTAGTGTCTAGAAAAAGTTGTGGTACAGTCTA 6348

QY 132 TTATGGGTACCTGTGTGAGAGAAAGCAACCACCTCTATTTTGTGCATCAGATGCTAA 191

Db 6349 TTATGGGTACCTGTGTGAAAGAAACAACCACCTCTATTTTGTGCATCAGATGCTAA 6408

QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251

Db 6409 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 6468

QY 252 CAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAATAA 311

Db 6469 CAACCCACAAGAAGTAGTATTGGGAAATGTAAACAGAAGATTTTAACATGTGGAAAAATAA 6528

QY 312 CATGGTAGATCAGATGCATCAGGATATAATCAGTTTATGGGATGAAAGCCTAAAAGCCATG 371

Db 6529 CATGGTAGAACAGATGCAGGAGGATGTAATCAATTTATGGGATCAAAGCTTAAAGCCATG 6588

QY 372 TGTAAATTAACCCCACTCTGTGTTACTTTAAATTTGCACATAATTGTAATATCACATAAGAA 431

Db 6589 TGTAAATTAACCCCACTCTGTGTTACTTTTAAATTTGCAAAGATGT-----GAA 6636

QY 432 TACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGAGAAAGGAGAAAAATAAAAAATTG 491

Db 6637 TGCTACTAATACCACCTAGTAGTAGTGAGGGAATGATGGAGAGAGGAGAAATAAAAACTG 6696

QY 492 CTCTTTCTATATCACCAAGCATAGAATAAGTAAAGAAAGAAATATGCACCTTTTAA 551

Db 6697 CTCTTTCAATATCACCAAAAGCATAGAATAAGGTGAGAGAAAGAAATATGCTCTTTTAA 6756

QY 552 TAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAATAAGTTG 611

Db 6757 TAACTGGATGTAGTACCAATAGATATAAAGAATAATACCAATATAGGTTAATAAGTTG 6816  
QY 612 TAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCAAATCCCATACA 671  
Db 6817 TAACACCTCAGTCATTACACAAGCCTGTCCAAAGGTATCCTTTGAACCAATCCCATACA 6876  
QY 672 TTATTGTGTCGGGCTGGGTTTGGCATGTGTAAGGTGAACAATAAGACATTCAATGGATC 731  
Db 6877 TTATTGTGCCCCGGCTGGTTTTCGGAATCTTAAAGTGTATAATAAGACATTCAATGGAAA 6936  
QY 732 AGGACCATGCACAAATGTAGCAGCAGTACAAATGTACACATGGAATTAGCCAGTGTGTC 791  
Db 6937 AGGACAATGTAAAAATGTAGCAGCAGTACAAATGTACACATGGAATTAGCCAGTAGTATC 6996  
QY 792 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGAAAA 851  
Db 6997 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGTTGTAATTAGATCTGACAA 7056  
QY 852 TTTCACAGACAATGCTAAAAACCATATATAGTACAGCTAAATGAATCTGTAGTAATTAATG 911  
Db 7057 TTTTACGGACAATGCTAAAAACCATATATAGTACAGCTGAATGAATCTGTAAAAATTAATG 7116  
QY 912 TACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACAGGGAGAGCATTTTA 971  
Db 7117 TACAAGGCCAGCAACAATAACAAGAAAAAGTATACATATAGGACAGGGAGAGCATTTTA 7176  
QY 972 TGCAAGAAGAAAAACATAATAGGAGATATAAGACAAGCACATTTGAACATTAGTAGAGCAA 1031  
Db 7177 TACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTTGAACATTAGTAGAGCACA 7236  
QY 1032 ATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAGAGAAAAATTTAGGAATAAAC 1091  
Db 7237 ATGGAATAACACTTTTACAACAGATAGTTGAAAAATTAAAGAGACAATTTAATAATAAAC 7296  
QY 1092 AATAGCTTTAATCAATCCTCAGGAGGGACCCAGAAATTGTAATGCACAGTTTAAATG 1151  
Db 7297 AATAGCTTTAATCAATCCTCAGGAGGGATCCAGAAATTGTAATGCACAGTTTAAATG 7356  
QY 1152 TGGAGGGGAATCTTCTACTGTATATACAGCACAACCTGTTTATAGTACTTGAATGTTAC 1211  
Db 7357 TGGAGGGGAATTTTCTACTGTATATCAACACAACCTGTTTATAGTACTTGAATGATAC 7416  
QY 1212 TGGAGGGCAAAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAGAAATAAAC 1271  
Db 7417 TGAAAAGTCAAGTGGCACTGAAGGAATGACACCATCATACTCCCATGCAGAAATAAAC 7476  
QY 1272 AATTATAAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGGACA 1331  
Db 7477 AATTATAAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCTCTCCCATTAAGGACA 7536  
QY 1332 AATTAGATGTTCAATCAATATTACAGGCTGCTACTAACAAGAGATGGAGGTAATAGTAC 1391  
Db 7537 AATTAGATGTTCAATCAATATTACAGGCTGCTATTAAACAAGAGATGGTGGTAA ---AAA 7593  
QY 1392 TGAGACTGAGACTGAGATCTTCAGACTGGAGGAGGAGATATGAGGGACAATTTGGAGAAG 1451  
Db 7594 TGAGAGTGAGATCGAGATCTTCAGACCTGGAGGAGGAGACATGAGGGACAATTTGGAGAAG 7653  
QY 1452 TGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCACAGGGC 1511  
Db 7654 TGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCACAGGGC 7713  
QY 1512 AAAGAGAAGACAGTGCAAGAGAGAAAAAGACCGGATCCAGAG 1556  
Db 7714 AAAGAGAAGAGTGGTGCAAGAGAGAAAAAGAGCAGTGGGAATAGG 7758

RESULT 14

ADP20074

ID ADP20074 standard; DNA; 9540 BP.

XX

AC ADP20074;

XX DT 09-SEP-2004 (first entry)  
XX DE Human immunodeficiency virus 1 isolate JRCSE nucleotide sequence.  
XX KW immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;  
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;  
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSE;  
KW gene; ds.  
XX OS Human immunodeficiency virus 1.  
XX FH Key Location/Qualifiers  
FT LTR 1..635  
FT FT /\*tag= a  
FT FT /partial  
FT FT 790..2304  
FT FT /\*tag= b  
FT FT /product= "gag"  
FT FT 2085..5108  
FT FT /\*tag= c  
FT FT /product= "pol"  
FT FT 5053..5631  
FT FT /\*tag= d  
FT FT /product= "vif"  
FT FT 5571..5861  
FT FT /\*tag= e  
FT FT /product= "vpr"  
FT FT 6073..6318  
FT FT /\*tag= f  
FT FT /product= "vpu"  
FT FT 6236..8782  
FT FT /\*tag= g  
FT FT /product= "env"  
FT FT 8784..9434  
FT FT /\*tag= h  
FT FT /product= "nef"  
FT FT 9103..9540  
FT FT /\*tag= i  
FT FT /partial  
XX WO2004053100-A2.  
XX PD 24-JUN-2004.  
XX PF 11-DEC-2003; 2003WO-US039534.  
XX PR 11-DEC-2002; 2002US-0432869P.  
XX PR 24-APR-2003; 2003US-0465350P.  
XX PA (SCRI ) SCRIPPS RES INST.  
XX PI Burton DR, Wilson I, Pantophlet R;  
XX WPI; 2004-480933/45.  
DR P-PSDB; ADP20067, ADP20068, ADP20069, ADP20070, ADP20071, ADP20072,  
DR ADP20073.  
DR GENBANK; M38429.  
XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against  
PT the polypeptide, useful preventing or treating human immunodeficiency  
PT virus (HIV) infection, especially HIV-1 infection.  
XX Disclosure; Page 139-141; 149pp; English.  
PS The present invention describes an immunogenic mutant HIV gp120  
XX polypeptide that can stimulate a neutralising antibody response against a  
CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic  
CC mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising  
CC antibody response against a panel of HIV-1 comprising HIV-1 primary  
CC isolates of at least two different clades, where the mutant gp120 has at  
CC least one amino acid mutation in at least one epitope of the HIV-1 gp120  
CC polypeptide specifically bound by a neutralising antibody, which reduces





KW envelope protein; ss.  
OS Human immunodeficiency virus 1.  
XX  
FH Key Location/Qualifiers  
FT CDS 394..476  
FT /\*tag= b  
FT /product= "rev"  
FT CDS 648..3215  
FT /\*tag= a  
FT /product= "env"  
XX  
PN USN7599491-N.  
XX  
PD 15-OCT-1991.  
XX  
PF 17-OCT-1990; 90US-00183830.  
XX  
PR 17-OCT-1990; 90US-00599491.  
XX  
PA (USSH ) NAT INST OF HEALTH.  
XX  
PI Reitz M;  
XX  
DR WPI; 1991-346752/47.  
DR P-PSDB; AAR14905.  
XX  
PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in  
PT therapeutics, vaccines and diagnostic tests.  
XX  
PS Example 3; Fig 8; 6lpp; English.  
XX  
CC A HindIII fragment of unintegrated viral DNA representing the HIV-1 (BA-  
CC L) genome was cloned by standard techniques into lambda phage Charon 28  
CC DNA from total DNA of peripheral blood macrophages infected with and  
CC producing HIV-1 (BA-L). A positive clone was selected by hybridisation  
CC using a HIV-1 envelope probe. This clone, designated BA-L1, contained the  
CC entire env gene. The insert was subcloned and sequenced. The BA-L plasmid  
CC clone has been deposited as ATCC 40890. The sequenced also contains the  
CC coding region for the rev protein which is needed for efficient  
CC expression of the envelope protein in eukaryotic cells. (Note: Revised  
CC entry submitted to correct the patent number format of US Government-  
CC owned NTIS applications to prevent clashes with ongoing US granted patent  
CC numbers. For further information please visit the Derwent web site at  
CC www.derwent.com/dwpi/updates/ntis us.html.) (Updated on 25-MAR-2003 to  
CC correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;  
  
Query Match 55.2%; Score 1219; DB 2; Length 3807;  
Best Local Similarity 89.7%; Pred. No. 8.2e-239;  
Matches 1335; Conservative 0; Mismatches 145; Indels 9; Gaps 2;  
  
QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAAATTGTGGGTCACAGTCTA 131  
Db |||||  
QY 132 TTATGGGTACCTGTGTGGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA 191  
Db |||||  
QY 761 TTATGGGTACCTGTGTGGAAAGCAACCACTCTATTTTGTGCATCAGATCGTAA 820  
QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251  
Db |||||  
QY 821 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 880  
QY 252 CAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA 311  
Db |||||  
QY 312 CATGGTATGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGCCTTAAAGCCATG 371  
Db |||||  
QY 941 CATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCCTTAAAGCCATG 1000

QY 372 TGTAAAAATAACCCCACTCTGTGTCTTAAATTCGACCTAAATTTGA-----ATATCAC 425  
Db |||||  
QY 1001 TGTAAAAATAACCCCACTCTGTGTCTTAAATTCGACCTAAATTTGAGGAATGCTACTAA 1060  
QY 426 TAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAA 485  
Db |||||  
QY 1061 TGGGAATGACACTAATACCACTAGTAGCAGGGGAATGGTGGGGGAGGAGAAATGAA 1120  
QY 486 AAATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACT 545  
Db |||||  
QY 1121 AAATTGCTCTTTCAATATACCAACAATAAGAGGTAAAGGTGCAGAAAGAAATATGCACT 1180  
QY 546 TTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAATAATCTAAGTATAGGTTAAT 605  
Db |||||  
QY 1181 TTTTATAAACTTGATATAGCACCAATAGATAATAATAGTAATAATAGATATAGGTTGAT 1240  
QY 606 AAGTTGTAACACCTCAGTCATTAACAGGCCCTGTCAAAAGGTATCCTTTAGCCCAATTC 665  
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QY 1241 AAGTTGTAACACCTCAGTCATTAACAGGCCCTGTCAAAAGGTATCCTTTAGCCCAATTC 1300  
QY 666 CATACATTATTGTGTCCTGGCTGGGTTTTCGATGCTTAAAGTGTAAACAATAAGACATTC 725  
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QY 1301 CATACATTATTGGTGCCCGGCTGGTTTTCGATTCCTTAAAGTGTAAAGATAAGAAGTTCAA 1360  
QY 726 TGGATCAGGACCATGCAAAATGTCAGCACAGTACATGTACACATGGAATTAGGCCAGT 785  
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QY 1361 TGGAAAAGGACCATGTACAAATGTCAGCACAGTACATGTACATGGAATTAGGCCAGT 1420  
QY 786 GGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATC 845  
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QY 1421 AGTATCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAGGTAGTAATTAGATC 1480  
QY 846 TGAATAATTTACAGACAAATGCTTAAACCATAATAGTACAGCTAAAATGAATCTGTAGTAAT 905  
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QY 1481 CGCCAATTTGCGGACAAATGCTAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540  
QY 906 TAATTGTACAAGACCCCAACAATAACAAGAAAGGTTATCTATAGGACCAGGAGAGC 965  
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QY 1541 TAATTGTACAAGACCCCAACAATAACAAGAAAGTATACATATAGGACCAGGAGAGC 1600  
QY 966 ATTTTATGAAGAAGAAACATAATAGGAGATATAAGCAAGCACATTTGTAACATTAGTAG 1025  
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QY 1601 ATTTTATACAACAGGAGAAATAATAGGAGATATAAGCAAGCACATTTGTAACCTTACTAG 1660  
QY 1026 AGCAAAATGGAATAACACTTTTACAACAGATAGTTTAAATAAGAGAAAAATTTAGGAA 1085  
Db |||||  
QY 1661 AGCAAAATCGAATGACACTTTTAAATAAGATAGTTTAAATAAGAAACAATTTTGGGAA 1720  
QY 1086 TAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGCCAGAAAAATTTGTAATGCACAGTTT 1145  
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QY 1721 TAAAACAATAGTCTTTAAGCACTCCTCAGGAGGGGCCAGAAAAATTTGTACGCACAGTTT 1780  
QY 1146 TAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTGGAA 1205  
Db |||||  
QY 1781 TAATTGTGGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAAATAGTACTTGGAA 1840  
QY 1206 TGTACTGGAGGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAGAAAT 1265  
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QY 1841 TGTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACACAATCACACTCCCATGCAGAAAT 1900  
QY 1266 AAAACAAATTTATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCCCTCCCATCAC 1325  
Db |||||  
QY 1901 AAAACAAATTTATAAACATGTGGCAGGAAGTAGGAAAGCAATGTATGCCCCCTCCCATCAG 1960  
QY 1326 AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAA 1385  
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QY 1961 AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--- 2017  
QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAAATTG 1445  
Db |||||  
QY 2018 TCCTGAGGACAAACAAGACCGAGGTCTTCAGACCTGGAGGAGAGATATGAGGGATAAATG 2077  
QY 1446 GAGAAAGTGAATTATATAATAATAAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCAC 1505

Db	2078	GAGAAAGTGAATTATATATAAATATAAAGTAGTAAAAATTGAACCATTTAGGAGTAGCACCCAC	2137
Qy	1506	CAGGGCAAAGAGAAGAACAGTGCAAAAGAGAAAAAAGACCGGATCCAAGA	1554
Db	2138	CAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATA	2186

Search completed: November 12, 2004, 01:29:34  
Job time : 733.277 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 128.864 Seconds  
(without alignments)  
12178.890 Million cell updates/sec

Title: US-09-687-864A-13  
Perfect score: 2208  
Sequence: 1 aagcttgccgccatgctgta.....aactcgagtataatctaga 2208

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents,NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225.8	55.5	3807	1 US-08-022-835-5	Sequence 5, Appli
2	1225.8	55.5	3807	1 US-08-388-809-5	Sequence 5, Appli
3	1225.8	55.5	3807	2 US-08-647-714-5	Sequence 5, Appli
c 4	1174.2	53.2	3807	2 US-08-417-210A-78	Sequence 78, Appl
c 5	1174.2	53.2	3807	4 US-09-136-159A-78	Sequence 78, Appl
6	1173	53.1	2552	2 US-08-448-603A-27	Sequence 27, Appl
7	1173	53.1	2552	3 US-09-134-075-27	Sequence 27, Appl
8	1173	53.1	2552	3 US-09-492-739-27	Sequence 27, Appl
9	1172.2	53.1	2571	1 US-08-254-358-3	Sequence 3, Appli
10	1172.2	53.1	2571	1 US-08-475-391-3	Sequence 3, Appli
11	1172.2	53.1	2571	2 US-08-709-609-3	Sequence 3, Appli
12	1172.2	53.1	2571	4 US-09-552-950-3	Sequence 3, Appli
13	1172.2	53.1	2571	4 US-09-936-572-3	Sequence 3, Appli
14	1172.2	53.1	2571	5 PCT-US95-07178-3	Sequence 3, Appli
c 15	1172.2	53.1	6474	3 US-08-651-472-66	Sequence 66, Appl
c 16	1172.2	53.1	6474	3 US-08-358-928-66	Sequence 66, Appl
17	1172.2	53.1	6926	3 US-08-651-472-69	Sequence 69, Appl
18	1172.2	53.1	6926	3 US-08-358-928-69	Sequence 69, Appl
19	1172.2	53.1	9739	1 US-08-022-835-1	Sequence 1, Appli
20	1172.2	53.1	9739	1 US-08-388-809-1	Sequence 1, Appli
21	1172.2	53.1	9739	2 US-08-647-714-1	Sequence 1, Appli
22	1172.2	53.1	9746	1 US-08-022-835-3	Sequence 3, Appli
23	1172.2	53.1	9746	1 US-08-388-809-3	Sequence 3, Appli
24	1172.2	53.1	9746	2 US-08-647-714-3	Sequence 3, Appli
25	1171.4	53.1	1539	3 US-07-956-483-21	Sequence 21, Appl
26	1171.4	53.1	1539	3 US-08-472-240A-13	Sequence 13, Appl
27	1169.8	53.0	2573	2 US-08-448-603A-29	Sequence 29, Appl

28	1169.8	53.0	2573	3 US-09-134-075-29	Sequence 29, Appl
29	1169.8	53.0	2573	3 US-09-492-739-29	Sequence 29, Appl
30	1168.8	52.9	4527	2 US-08-944-449-8	Sequence 8, Appli
31	1168.8	52.9	4527	3 US-09-353-362-8	Sequence 8, Appli
32	1168.6	52.9	1532	2 US-08-037-816A-15	Sequence 15, Appl
33	1168.6	52.9	1532	2 US-08-530-146-15	Sequence 15, Appl
34	1165.4	52.8	1532	2 US-08-037-816A-27	Sequence 27, Appl
35	1165.4	52.8	1532	2 US-08-530-146-27	Sequence 27, Appl
36	1161.8	52.6	1932	4 US-09-475-515-31	Sequence 31, Appl
37	1161.8	52.6	2457	4 US-09-475-515-32	Sequence 32, Appl
38	1161.6	52.6	2570	2 US-08-448-603A-31	Sequence 31, Appl
39	1161.6	52.6	2570	3 US-09-134-075-31	Sequence 31, Appl
40	1161.6	52.6	2570	3 US-09-492-739-31	Sequence 31, Appl
41	1161	52.6	1419	4 US-09-475-515-30	Sequence 30, Appl
42	1160.8	52.6	9737	2 US-08-944-449-7	Sequence 7, Appli
43	1160.8	52.6	9737	3 US-09-353-362-7	Sequence 7, Appli
44	1160.4	52.6	1929	4 US-09-602-864-12	Sequence 12, Appl
45	1160	52.5	1527	3 US-07-956-483-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-08-022-835-5  
; Sequence 5, Application US/08022835  
; Patent No. 5420030  
; GENERAL INFORMATION:  
; APPLICANT: Reitz Jr., Marvin S.  
; APPLICANT: Franchini, Genoveffa  
; APPLICANT: Markham, Phillip D.  
; APPLICANT: Gallo, Robert C.  
; APPLICANT: Lori, Franco C.  
; APPLICANT: Popovic, Mikulas  
; APPLICANT: Garnter, Suzanne  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/022,835  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scott, Watson T.  
; REGISTRATION NUMBER: 26,581  
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3807 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS



; LOCATION: 648..3215									
US-08-022-835-5									
Query Match		55.5%	Score	1225.8;	DB	1;	Length	3807;	
Best Local Similarity		89.9%	Pred.	No. 1.3e-289;					
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QY	72	CATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAAATTGTGGGTCACAGTCTA	131						
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QY	132	TTATGGGTACCTGTGTGGAGAGAAACAACCACCTCTATTTTGTGCATCAGATGCTAA	191						
Db	761	TTATGGGTACCTGTGTGGAAAGAAGCAACCACCTCTATTTTGTGCATCAGATCGTAA	820						
QY	192	AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC	251						
Db	821	AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC	880						
QY	252	CAACCCACAAGAAGTAGTATTGGGAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA	311						
Db	881	CAACCCACAAGAAGTAGAATTGAAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA	940						
QY	312	CATGGTAGATCAGATGATAGAGGATATAATCAGTTTATGGGATGAAAGCCTTAAAGCCATG	371						
Db	941	CATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCCTTAAAGCCATG	1000						
QY	372	TGFAAAATTAACCCCACTCTGTGTTACTTTAAATTGCACCTAAATTTGA-----ATATCAC	425						
Db	1001	TGFAAAATTAACCCCACTCTGTGTTACTTTAAATTGCACCTGATTTGAGGAATGCTACTAA	1060						
QY	426	TAAGAACTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAGAAAGGAGAAATAAA	485						
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QY	486	AAATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCAC	545						
Db	1121	AAATTGCTCTTTCAATATACCACAAAACATAAGAGGTAAAGGTGCAGAAAGAAATATGCAC	1180						
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QY	786	GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTAGATC	845						
Db	1421	AGTATCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAGGTAGTAATTAGATC	1480						
QY	846	TGAAAAATTCACAGACAATGCTFAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT	905						
Db	1481	CGCCAAATTCGGGACAATGCTFAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT	1540						
QY	906	TAATTGTACAAGACCCCAACAATAACAAGAAAGGTTATCTATAGGACCCAGGGAGAGC	965						
Db	1541	TAATTGTACAAGACCCCAACAATAACAAGAAAGTATACATATAGGACCCAGGCAGAGC	1600						
QY	966	ATTTTATGAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG	1025						
Db	1601	ATTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACCTTAGTAG	1660						
QY	1026	AGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAA	1085						

Db	1661	AGCAAAATGGAATGACACTTTAAATAAGATAGTTATAAAATTAAGAGAACAATTTGGGAA	1720
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Db	1721	TAAAACAATAGTCTTTAAGCACTCCTCAGGAGGGACCCAGAAAATTGTGACGCACAGTTT	1780
QY	1146	TAATTGTGGAGGGAAATCTTCTACTGTAATACAGCAAACTGTTTAAATAGTACTTTGGAA	1205
Db	1781	TAATTGTGGAGGGAAATTTTCTACTGTAATTCACACAACACTGTTTAAATAGTACTTTGAA	1840
QY	1206	TGTTACTGGAGGACAAAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAGAAAT	1265
Db	1841	TGTTACTGAAGAGTCAAATAACACTGTAGAAAATAACAACATCACACTCCCATGCAGAAAT	1900
QY	1266	AAAACAAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC	1325
Db	1901	AAAACAAAATTATAACATGTGGCAGGAAGTAGGAAAGAGCAATGTATGCCCTCCCATCAG	1960
QY	1326	AGGACAAATTAGATGTTCAATAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAA	1385
Db	1961	AGGACAAATTAGATGTTCAATAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG---	2017
QY	1386	TAGTACTGAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGAGATATGAGGGACAATTG	1445
Db	2018	TCCTGAGGACAACACAGACCGAGGTCTTCAGACCTCGAGGAGGAGATATGAGGGATAATTG	2077
QY	1446	GAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCAC	1505
Db	2078	GAGAAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCAC	2137
QY	1506	CAGGGCAAAGAGAAACACAGTGTCAAAGAGAAAAAGACCGGATCCAAGAAG	1556
Db	2138	CAAGGCAAAGAGAGAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGG	2188

RESULT 2

US-08-388-809-5  
; Sequence 5, Application US/08388809  
; Patent No. 5576000  
; GENERAL INFORMATION:  
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI.  
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT  
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
; APPLICANT: GARTNER, SUZANNE  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK, 3.5"  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,809  
; FILING DATE: 15-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,835  
; FILING DATE: 25-FEB-1993  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LESLIE A. SERUNIAN  
; REGISTRATION NUMBER: 35,353  
; REFERENCE/DOCKET NUMBER: 2026-4092US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800







ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,210A  
FILING DATE: 05-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
. NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2690  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-840-3333  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3807 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-417-210A-78

Query Match 53.2%; Score 1174.2; DB 2; Length 3807;  
Best Local Similarity 88.1%; Pred. No. 5e-277;  
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

Qy	52	TGGATCTCGGCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
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Qy	112	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA	171
Db	1608	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTA	1549
Qy	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	1548	TTTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT	1489
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAT	291
Db	1488	GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGAATTGGTAAATGTGACAGAAAT	1429
Qy	292	TTTAAACATGTGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
Db	1428	TTTAAACATGTGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGG	1369
Qy	352	GATGAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	411
Db	1368	GATCAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	1309
Qy	412	AATTG-----AATATCACTAAGAAATACTACTAATCCCACCTAGTAGCAGCTGG	459
Db	1308	GATTTGAGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAAGTAAATAGCGAG	1249
Qy	460	GGAAATGATGGAGAAAGGAGAAATAAAAAAATTGCTCTTTCTATATCACCAAGCATAAGA	519
Db	1248	GGAACAATAAAGGGAGAGAAATGAAAAAATGCTCTTTCAATATCACCAAGCATAAGA	1189
Qy	520	AATAAGGTAAAGAAAGATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAT	579
Db	1188	GATAAGATGCAGAAAGAAATATGCACTCTTTATAAACTTGATATAGTATCAAT--AAAT	1132
Qy	580	ACTAATAATACTAAGTATAGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGT	639
Db	1131	AATGATAGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT	1072
Qy	640	CCAAAGGTATCCTTTTCAGCCAAATTCACATACATTATTGTGTCGGCTGGTTTGCATG	699
Db	1071	CCAAAGATATCCTTTTGAGCCAAATTCACATACACTATTGTGCCCGGCTGGTTTGCATT	1012

Qy	700	CTAAAGTGTAACAATAAGACATTCAATGGATCAGGACCATGCACAAATGTCTCAGCACAGTA	759
Db	1011	CTAAAGTGTAACGATAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAATGTCTCAGCACAGTA	952
Qy	760	CAATGTACACATGGAATTAGCCAGTGGTGTCAACTCAACTGCTGTCTTAAATGGCAGTCTA	819
Db	951	CAATGTACACATGGAATTAGCCAGTAGTATCAACTCAACTGCTGTCTTAAATGGCAGTCTA	892
Qy	820	GCAGAAGAAGACATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATA	879
Db	891	GCAGAAGAAGAGGTAGTAATTAGATCTGAGAATTTCAATGATAATGCTAAAAACCATATA	832
Qy	880	GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCACAAACAATAACAAGAAGA	939
Db	831	GTACATCTGAATGAATCTGTACAAAATTAATTGTACAAGACCACCAACTACAATAAAGAAAA	772
Qy	940	AGTTTATCTATAGGACCAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATA	999
Db	771	AGGATACATATAGGACCAGGAGAGCATTTTATACAACAAAAAATAATAGGAACATA	712
Qy	1000	AGACAAGCACATTGTAAACATTAGTAGAGCAAAAATGGAATTAACACTTTACAACAGATAGTT	1059
Db	711	AGACAAGCACATTGTAAACATTAGTAGAGCAAAAATGGAATGAACACTTTAAGACAGATAGTT	652
Qy	1060	ATAAAATTAAAGAGAAAAATTTAGGAATAAAAAACAATAGCCCTTTAATCAATCCTCAGGAGG	1119
Db	651	AGCAAAATTAAAGAAACAATTTAAGAATAAAAAACAATAGTCTTTAATCAATCCTCAGGAGG	592
Qy	1120	GACCCAGAAAATTGTAATGCAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAAATACA	1179
Db	591	GACCCAGAAAATTGTAATGCAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAAATCA	532
Qy	1180	GCACAACTGTTTAAATAGTACTTGAATGTTTACTTGGAGGGCAAAAATGGCACTGAAGG--A	1236
Db	531	TCACCACTGTTTAAATAGTACTTGAATGTTTAAATAATACTTGGAAATAATACTACAGGTC	472
Qy	1237	AATGACATAATCACACTCCAATGCAGAAATAAAACAATAATAATAATATGGCAGAAAGTA	1296
Db	471	AATAACAATATCACACTTCAATGCAAAATAAAACAATAATAACATGTGGCAGGAAGTA	412
Qy	1297	GGAAAAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATTTACA	1356
Db	411	GGAAAAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAATATTTACA	352
Qy	1357	GGGCTGCTACTAACAGAGATGGAGGTAAATAGTACTGA--GACTGAGACTGAGATCTTC	1413
Db	351	GGGCTACTATTAAACAAGAGATGGTGGTAAGGACACGGACACGACACCGAGATCTTC	292
Qy	1414	AGACCTGGAGGAGGAGATATAGGGGACAAATTTGGAGAGTGAATTTATATAATATAAAGTA	1473
Db	291	AGACCTGGAGGAGGAGATATAGGGGACAAATTTGGAGAGTGAATTTATATAATATAAAGTA	232
Qy	1474	GTAAGAAATTGAACCAATAGGAGTAGCACCCACCCAGGGGCAAGAGAGAAAGACAGTGCAAGA	1533
Db	231	GTAACAATTGAACCATTAGGAGTAGCACCCACCCAGGCAAGAGAGTGGTGCAGAGA	172
Qy	1534	GAATAAAGA 1542	
Db	171	GAATAAAGA 163	

RESULT 5  
US-09-136-159A-78/c  
; Sequence 78, Application US/09136159A  
; Patent No. 6596279  
; GENERAL INFORMATION:  
; APPLICANT: Virogenetics Corporation  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Tartaglia, James  
; APPLICANT: Cox, William I  
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus  
; FILE REFERENCE: 454310-2690.1  
; CURRENT APPLICATION NUMBER: US/09/136,159A

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; CURRENT FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-09-136-159A-78
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Query Match          53.2%;   Score 1174.2;   DB 4;   Length 3807;
Best Local Similarity 88.1%;   Pred. No. 5e-277;
Matches 1330;   Conservative 0;   Mismatches 158;   Indels 21;   Gaps 4;
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QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1668 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 1609

QY 112 AAATTGTGGGTCACAGCTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1608 AAATTGTGGGTCACAGCTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTA 1549

QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1548 TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489

QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTTGGGAAATGTGACAGAAAAT 291
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGAATTGGTAAATGTGACAGAAAAT 1429

QY 292 TTTTAACATGTGGAAAAATAACATGGTGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1428 TTTTAACATGTGGAAAAATAACATGGTGTAGAACAGATGCATGAGGATATAATCAGTTTATGG 1369

QY 352 GATGAAAGCCTAAAGCCATGTGTAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACT 411
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1368 GATCAAAGCCTAAAGCCATGTGTAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACT 1309

QY 412 AATTG-----AATATCACTAAGAATACTACTAATCCCACCTAGTAGCAGCTGG 459
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1308 GATTGAGGAATACTACTAATACCAATAATAGTACTGTCTAATAAACCAATAGTAATAGCGAG 1249

QY 460 GGAATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTPATATCACCACAAGCATAAAGA 519
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1248 GGAACAATAAAGGGAGAGAAATGAAAAAATGCTCTTTTCAATATCACCACAAGCATAAAGA 1189

QY 520 AATAAGGTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTATAGTACCAATAGAAAAT 579
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1188 GATAAGATGCAGAAAGAATATGCACTTCTTTATAAATCTTGATATAGTATCAAT---AAAT 1132

QY 580 ACTAATAACTAAGTATAGTTAATAAGTTGTAACACCTCAGTCATTACAGGCGCTGT 639
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1131 AATGATAGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT 1072

QY 640 CCAAAGGTATCCTTTTCAGCCCAATTCCCATACATTATTGTGTCCCGGCTGGTTTGGCATG 699
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RESULT 6
US-08-448-603A-27
; Sequence 27, Application US/08448603A
; Patent No. 5864027
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
```

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Db 1071 CCAAAGATATCCTTTGAGCCAATTTCCCATACACTATTGTGCCCCGGCTGGTTTTCGCAAT 1012

QY 700 CTAAAGTGTAACAATAAAGACATTCAATGGATCAGGACCATGTGCAAAAATGTCAGCACAGTA 759
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1011 CTAAAGTGTAACGATAAAAAAGTTTCAGTGGAAAAAGGATCATGTAAAAATGTCAGCACAGTA 952

QY 760 CAATGTACACATGGAATTAGGCCAGTGGTGTCACACTCAACTGCTGTTAAATGGCAGTCTA 819
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 951 CAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA 892

QY 820 GCAGAAAGAAGACATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAAACCATAATA 879
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 891 GCAGAAAGAAGAGGTAGTAATTAGATCTGAGAATTTCAATGATAATGCTAAAAACCATCATA 832

QY 880 GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGA 939
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 831 GTACATCTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAAAAGAAA 772

QY 940 AGGTTATCTATAGCACGAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATA 999
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 771 AGGATACATATAGGACCAGGGAGAGCATTTTATACAACAAAAAAATATAATAGGAACTATA 712

QY 1000 AGACAAAGCACATTTGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTT 1059
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 711 AGACAAAGCACATTTGTAACATTAGTAGAGCAAAATGGAATGACACTTTAAGACAGATAGTT 652

QY 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGGG 1119
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 651 AGCAAAATTAAGAAACAATTTAAGAAATAAAAAACAATAGTCTTTAATCAATCCTCAGGAGGG 592

QY 1120 GACCCAGAAAATTTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAATACA 1179
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 591 GACCCAGAAAATTTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAATCA 532

QY 1180 GCACAACTGTTTAAATAGTACTTGGAAATGTTTACTGGAGGGAACAATGGCACTGAAGG--A 1236
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 531 TCACCACTGTTTAAATAGTACTTGGAAATGTTAATACTTGGAAATAATACTACAGGTCA 472

QY 1237 AATGACATAATCACACTCCAATGCAGAATAAAAAACAATAATAAAATATGTGGCAGAAAGTA 1296
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 471 AATAACAATATCACACTTCAATGCAAAATAAAAAACAATAATAAAACATGTGGCAGGAAGTA 412

QY 1297 GGAAGAAGCAATGTATGCCCTCCCCTCACAGGACAAATTAGATGTTTCATCAAAATATTACA 1356
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 411 GGAAGAAGCAATATATGCCCTCCCCTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA 352

QY 1357 GGGCTGCTACTAAACAAGAGATGGAGGTAAATAGTACTGA--GACTGAGACTGAGATCTTC 1413
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 351 GGGCTACTATTAAACAAGAGATGGTGTAGGACACGGACACGAACGACCCGAGATCTTC 292

QY 1414 AGACCTGGAGGAGGAGATATAGGGGACAAATTGGAGAAAGTGAATTATATAAATATAAAGTA 1473
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 291 AGACCTGGAGGAGGAGATATAGGGGACAAATTGGAGAAAGTGAATTATATAAATATAAAGTA 232

QY 1474 GTAAGAATTTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAAAGAACAGTGCAAGA 1533
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 GTAACAATTTGAACCAATTAGGAGTAGCACCCACCACCAAGGCAAGAGAGAGTGGTGCAGAGA 172

QY 1534 GAAAAAAGA 1542
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Db 171 GAAAAAAGA 163
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```

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
STREET: 3 Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,603A  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/072,833  
FILING DATE: 07-JUN-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Haliday, Emily  
REGISTRATION NUMBER: 38903  
REFERENCE/DOCKET NUMBER: 14918-704  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2552 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2552  
US-08-448-603A-27

Query Match 53.1%; Score 1173; DB 2; Length 2552;  
Best Local Similarity 88.8%; Pred. No. 8.5e-277;  
Matches 1337; Conservative 0; Mismatches 135; Indels 33; Gaps 5;

Qy	64	TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC	123
Db	46	TGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGAGAAAAATTGTGGGTC	105
Qy	124	ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCTCTATTTTGTGCATCA	165
Qy	184	GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC	243
Db	166	GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC	225
Qy	244	ACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGCAGAAAAATTTTAACATGTGG	303
Db	226	ACAGACCCCAACCCACAAGAAATAGGATTGGAAATGTACAGAAAAATTTTAACATGTGG	285
Qy	304	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
Db	286	AAAAATAACATGGTAGACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCTTA	345
Qy	364	AAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTTAATTTGACATAATTTGAATATC	423
Db	346	AAGCCATGTGTAATAATTAACCCACTATGTGTACTTTTAATTTGACATGATTTG-----	399
Qy	424	ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA	483
Db	400	---AAAAATGCTACTAATACCCTAGTAGCAGCTGGGGAAGATGGAGAGAGGAGAAATA	456
Qy	484	AAAAATTGCTCTTTCTATATCACCACAAGCATAGAATAAAGTAAGTTAAAGAAATATGCA	543
Db	457	AAAACTGCTCTTTCAATGTCAACCACAAGTATAAGAGATAAGATGAAGAATGAATATGCA	516

Qy	544	CTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAATAATACTAAGTATAGTTA	603
Db	517	CTTTTAAATAGACTTGATGTAGTACCAATAG---ATAATGATAATACTAGTATAGTTG	573
Qy	604	ATAAGTTGTAAACACCTCAGTCATTAACACAGGCCCTGTCCAAAGGTATCCTTTAGCCAAAT	663
Db	574	ATAAGTTGTAAACACCTCAGTCATTAACACAGGCCCTGTCCAAAGGTGTCTTTGAGCCAAAT	633
Qy	664	CCCATACATTATTGTGTCCTCCGGCTGGGTTTTCGATGCTTAAAGTGTAAACAATAAGACATTC	723
Db	634	CCCATACATTATTGTGTCCTCCGGCTGGTTCGATGCTTAAAGTGTAGAGATAAAAAGTTTC	693
Qy	724	AATGGATCAGGACCATGCACAAATGTCAGCACACAGTACATGTACACATGGAATTAGGCCA	783
Db	694	AACGGAACAGGACCATGTACAAATGTCAGCACAGTACATGTACACATGGAATTAGGCCA	753
Qy	784	GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA	843
Db	754	GTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAAAGAAAGTAGTAATTAGA	813
Qy	844	TCTGAAAAATTTACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTA	903
Db	814	TCTGCCAATTTCTCGGACAATGCTAAAAACCATAATAGTACAGCTGAACGAATCTGTAGAA	873
Qy	904	ATTAATTTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGA	963
Db	874	ATTAATTTGTACAAGACCCCAACAACAATACAAGAAAGTATACATATAGGACCAGGGAGA	933
Qy	964	GCATTTTATGCAAGAAACATATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGT	1023
Db	934	GCATTTTATGCAACAGGAGAAATATAGGAGACATAAGACAAGCACATTGTAAACCTTAGT	993
Qy	1024	AGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGG	1083
Db	994	AGCACAAAATGGAATAATACTTTAAAAACAGATAGTTACAAAATTAAGAGAACATTTT---	1050
Qy	1084	AATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCAGAAAAATTTGTAATGCACAGT	1143
Db	1051	AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGCCAGAAAAATTTGTAATGCACAGT	1110
Qy	1144	TTTAATTTGTGAGGGGAATTTCTTACTGTAATACAGCACAACTGTTTAATAGTACTTTGG	1203
Db	1111	TTTAATTTGTGAGGGGAATTTTCTACTGTAATACAAACCACCTGTTTAATAGTACTTTGG	1170
Qy	1204	AATGTTACTGGAGGGACAAATGGCACCTGAAGGAAATGA-----CATAATCACA	1251
Db	1171	AATTACTTATCTTGGAAATAACTGAAGGGTCAATGACACTGGAAGAAATATATCACA	1230
Qy	1252	CTCCAATGCAGAATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTAT	1311
Db	1231	CTCCAATGCAGAATAAAACAAATTATAAACATGTGGCAGGAAAGTAGGAAAAGCAATGTAT	1290
Qy	1312	GCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA	1371
Db	1291	GCCCCCTCCCATAGAGGACAAATTAGATGCTCATCAAATATTACAGGGCTGCTATTAAACA	1350
Qy	1372	AGAGATGGAGGTAAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAGAT	1431
Db	1351	AGAGATGGTGGTAATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAGAT	1404
Qy	1432	ATGAGGGACAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTTGAACCAATA	1491
Db	1405	ATGAGGGACAATTGGAGAACTGAATTATATAAATATAAAGTAGTAAGAATTTGAACCAATA	1464
Qy	1492	GGAGTAGCACCCACCAGGCAAGAGAAACACAGTGTGAAAAGAGAAAAAGACCCGGATCCA	1551
Db	1465	GGAGTAGCACCCACCAGGCAAGAGAAAGAGAGTGTATGCAGAGAGAAAAAGAGCAGTGGGA	1524
Qy	1552	AGAAG	1556
Db	1525	ATAGG	1529





Db 1405 ATGAGGACAAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTA 1464  
Qy 1492 GGAGTAGCACCACCAGGGCAAGAGAAAGACAGTGCAAGAGAAAAAGACCGGATCCA 1551  
Db 1465 GGAGTAGCACCACCACCAAGGCAAGAGAAAGAGTGATGCAGAGAAAAAAGAGCAGTGGGA 1524  
Qy 1552 AGAAG 1556  
Db 1525 ATAGG 1529

RESULT 8  
US-09-492-739-27  
; Sequence 27, Application US/09492739  
; Patent No. 6331404  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; Nakamura, Gerald R.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
; STREET: 3 Embarcadero Center  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/492,739  
; FILING DATE: 27-Jan-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/134,075  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haliday, Emily  
; REGISTRATION NUMBER: 38903  
; REFERENCE/DOCKET NUMBER: 14918-704  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-393-2000  
; TELEFAX: 415-393-2286  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2552 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2552  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-492-739-27

Query Match 53.1%; Score 1173; DB 3; Length 2552;  
Best Local Similarity 88.8%; Pred. No. 8.5e-277;  
Matches 1337; Conservative 0; Mismatches 135; Indels 33; Gaps 5;  
Qy 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC 123  
Db 46 TGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTGCAGAAAAATTGTGGGTC 105  
Qy 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACCTCTATTTTGTGCATCA 183  
Db 106 ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCACCTCTATTTTGTGCATCA 165

'Qy 184 GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 243  
Db 166 GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 225  
Qy 244 ACAGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303  
Db 226 ACAGACCCCAACCCACAAGAAATAGGATTGGAAATGTAAACAGAAAAATTTTAAACATGTGG 285  
Qy 304 AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363  
Db 286 AAAAATAACATGGTAGAAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCTTA 345  
Qy 364 AAGCCATGTGTAATAATAACCCCACTCTGTGTTACTTTTAAATTGCACTAATTTGAATATC 423  
Db 346 AAGCCATGTGTAATAATAACCCCACTATGTGTTACTTTTAAATTGCACTGATTTG----- 399  
Qy 424 ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATA 483  
Db 400 --AAAAATGCTACTATAATACCACCTAGTAGCAGCTGGGAAAGATGGAGAGAGGAGAAATA 456  
Qy 484 AAAAATTGCTCTTTCTATATCACCAAGCATAGAATAAGGTAAGGTAAGAAAGAAATATGCA 543  
Db 457 AAAAATGCTCTTTCAATGTCAACCAAGTATAAGAGATAAGATGAAGAATGAATATGCA 516  
Qy 544 CTTTTTAATAGACTTGATGTAGTACCAATAGAAAATACTAATAATACTAAGTATAGGTTA 603  
Db 517 CTTTTTATAAACTTGATGTAGTACCAATAG---ATAATGATAATACTAGCTATAGGTTG 573  
Qy 604 ATAAAGTTGTAACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCCTTTCAGCCCAAT 663  
Db 574 ATAAAGTTGTAACACCTCAGTCATTACACAGGCGCTGTCCAAAGGTGTCTTTGAGCCCAAT 633  
Qy 664 CCCATACATTATTGTGCCCGGCTGGTTTCGATGCTTAAAGTGTAAACAATAAGACATTC 723  
Db 634 CCCATACATTATTGTGCCCGGCTGGTTTCGATTTCTAAAGTGTAGAGATAAAAAAGTTTC 693  
Qy 724 AATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTTAGGCCA 783  
Db 694 AACGGAACAGGACCATGTACAAATGTGAGCACAGTACAATGTACACATGGAATTTAGGCCA 753  
Qy 784 GTGGTGTCAACTCAACTGCTGTTAAATGGCAGCTCTAGCAGAAAGACATAGTAATTAGA 843  
Db 754 GTAGTATCAACTCAACTGCTGTTAAATGGCAGTTTAGCAGAAAGAAAGTAGTAATTAGA 813  
Qy 844 TCTGAAAAATTTACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTA 903  
Db 814 TCTGCCAATTTCTCGGACAATGCTAAAACCATAATAGTACAGCTGAACGAATCTGTAGAA 873  
Qy 904 ATTAATTGTACAAGACCCAAACAATAACAAGAGAGGTTATCTATAGGACCAGGGAGA 963  
Db 874 ATTAATTGTACAAGACCCAAACAATAACAAGAGAGTATACATATAGGACCAGGGAGA 933  
Qy 964 GCATTTTATGCAAGAAACATATAAGGAGATATAAGACAAGCACATTTGTAACATTAGT 1023  
Db 934 GCATTTTATGCAACAGGAGAAATAATAGGAGACATAAGACAAGCACATTTGTAACCTTAGT 993  
Qy 1024 AGAGCAAAATGGAAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGG 1083  
Db 994 AGCACAAAATGGAAATAACTTTTAAAACAGATAGTTTACAAAATTTAAGAGAACATTTT--- 1050  
Qy 1084 AATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTTGTAATGCACAGT 1143  
Db 1051 AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGACCCAGAAAATTTGTAATGCACAGT 1110  
Qy 1144 TTTAATTGTGGAGGGGAATTTCTTACTGTAATACAGCACAACTGTTTTAATAGTACTTGG 1203  
Db 1111 TTTAATTGTGGAGGGGAATTTTCTACTGTAATACAAACACCACCTGTTTTAATAGTACTTGG 1170  
Qy 1204 AATGTTACTGGAGGGACAAATGGCAGTGAAGGAATGA-----CATAATCACA 1251  
Db 1171 AATTATACTTATCTTGAATAATACTGAAGGGTCAATGACACTGGAAGAAATATCACA 1230  
Qy 1252 CTCCAATGCAGAATAAAAACAAAATTATAAATATGTGCCAGAAAGTAGGAAAAAGCAATGTAT 1311

Db 1231 CTCCAATGCAGATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCCAATGTAT 1290  
Qy 1312 GCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACA 1371  
Db 1291 GCCCCTCCCATAGAGGACAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTAAACA 1350  
Qy 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431  
Db 1351 AGAGATGGTGGTAATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAGAT 1404  
Qy 1432 ATGAGGGACAAATTGGAGAGTGAATTATATAAAATATAAAAGTAGTAAGAATTGAACCAATA 1491  
Db 1405 ATGAGGGACAAATTGGAGAGTGAATTATATAAAATATAAAAGTAGTAAAAATTGAACCATTA 1464  
Qy 1492 GGAGTAGCACCACCAGGGCAAGAGAGAACACAGTGCAAAAGAGAAAAAGACCGGATCCA 1551  
Db 1465 GGAGTAGCACCACCACCAAGGCAAGAGAGAGTGATGCGAGAGAGAAAAAGAGCAGTGGGA 1524  
Qy 1552 AGAAG 1556  
Db 1525 ATAGG 1529

RESULT 9

US-08-254-358-3  
; Sequence 3, Application US/08254358  
; Patent No. 5658785  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,358  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5658785and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-254-358-3

Query Match 53.1%; Score 1172.2; DB 1; Length 2571;  
Best Local Similarity 87.9%; Pred.No. 1.3e-276;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117  
Db 40 TGGGATGGGGCACGATGCTCCTTGGGTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99

Qy 118 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACCTCTATTTTGT 177  
Db 100 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCACCTCTATTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAAGAAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAC 279  
Qy 298 ATGTGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357  
Db 280 ATGTGAAAAATAACATGGTAGAACAGATGATGAGGATATAATCAGTTTATGGGATCAA 339  
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACTAATTG 417  
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACGTGATTG 399  
Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTTAATAACAATAGTAATAGCGAGGGAACA 459  
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAG 525  
Db 460 ATAAAGGGAGGAGAAATGAAAAAACTGCTCTTTCAATATCACCAAGCATAAAGAGATAAG 519  
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGAATGTAGTACCAATAGAAAAATACTAAT 585  
Db 520 ATGCAGAAAGAAATATGCACCTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT 576  
Qy 586 AATACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAG 645  
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAAGCTTGTCCAAAG 636  
Qy 646 GTATCCTTTTCAGCCCAATTCCCATACATTATTGTGCCGGCTGGGTTTGCAGATGCTAAAAG 705  
Db 637 ATATCCTTTGAGCCCAATTCCCATACACTATTGTGCCCGCGCTGGTTTTCGATTCTAAAA 696  
Qy 706 TGTAAACAATAAGACATTCATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGT 765  
Db 697 TGTAAACGATAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTCAGCACAGTACATGT 756  
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 825  
Db 757 ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 816  
Qy 826 GAAGACATAGTAATTAGATCTGAAAAATTTTACAGACAATGCTAAAAACCATATAATAGTACAG 885  
Db 817 GAAGAGGTAGTAATTAGATCTGAGAATTTTCACTGATAATGCTAAAAACCATCATAGTACAT 876  
Qy 886 CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTA 945  
Db 877 CTGAATGAATCTGTACAATTAATTGTACAAGACCCCACTACAATAAAAAGAAAAAGGATA 936  
Qy 946 TCTATAGGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACCAGGGAGAGCATTTTATACAACAACAAAAATATAATAGGAACATAAGACAA 996  
Qy 1006 GCACATTGTAACTATTAGTAGCAAAAAATGGAATAACACTTTACAACAGATAGTTATAAAA 1065  
Db 997 GCACATTGTAACTATTAGTAGCAAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056  
Qy 1066 TTAAGAGAAAAAATTTAGGAATAAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCA 1125  
Db 1057 TTAAGAGAAACAAATTTAAGAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGGACCCA 1116  
Qy 1126 GAAATTGTAATGCACAGTTTAAATTTGGAGGGGAATTTCTTACTGTAAATACAGCACAA 1185  
Db 1117 GAAATTGTAATGCACAGTTTAAATTTGGAGGGGAATTTTCTACTGTAAATACATCACCA 1176



QY 1186 CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242  
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QY 1243 AFAATCACACTCCAATGCAGATAAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAA 1302  
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Db 1237 AATATCACACTTCAATGCAAAATAAAAACAAATTATAAACAATGTGGCAGGAAGTAGGAAAA 1296  
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QY 1303 GCAATGTATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362  
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Db 1297 GCAATGTATGCCCCCTCCCATTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356  
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QY 1363 CTACTAACAAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACCT 1419  
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Db 1357 CTATTAAACAAGAGATGGTGGAAGGACACCGGACACGAAACGACACCGAGATCTTTCAGACCT 1416  
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QY 1420 GGAGGAGGAGATATGAGGGACAATTGGAGAAAGTGAAATTATATAAATATAAAAGTAGTAAGA 1479  
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QY 1480 ATTGAACCAATAGGAGTAGCACCCACAGGGCAAGAGAAAGAACAGTGCACAAAGAGAAAAA 1539  
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Db 1477 ATTGAACCATTAGGAGTAGCACCCACCAAGGCAAGAGAAAGAGAGTGGTGCAGAGAGAAAAA 1536  
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QY 1540 AGACCGGATCCAAGA 1554  
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Db 1537 AGACGAGGATAGGA 1551  
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RESULT 10  
US-08-475-391-3  
; Sequence 3, Application US/08475391  
; Patent No. 5786211  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; FILING DATE: 08/254,358  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 578621land, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-475-391-3

Query Match 53.1%; Score 1172.2; DB 1; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 1.3e-276;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
  
QY 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117  
|||  
Db 40 TGGGGATGGGCACGATGCTCCTTGGGTATTATATGATCTGTAGTGTACAGAAAAATTG 99  
|||  
QY 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTATTGT 177  
|||  
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGCAACCACTCTATTATTGT 159  
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QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACATGCCTGT 237  
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Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTGGGCCACACAGCCTGT 219  
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QY 238 GTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297  
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Db 220 GTACCCACAGACCCCAACCCCAAGAAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAC 279  
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QY 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357  
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Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339  
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QY 358 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAAATTG 417  
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Db 340 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTGATTG 399  
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QY 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
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QY 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAATAAAG 525  
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QY 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAAT 585  
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QY 586 AATACTAAGTATAGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAG 645  
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Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAAG 636  
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QY 646 GTATCCTTTTCAGCCCAATTCCTATACATATTATGTGTCCTGGCTGGTTTTCGATGCTAAAG 705  
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Db 637 ATATCCTTTGAGCCCAATTCCTATACACTATTGTGTCCTGGCTGGTTTTCGATTTCTAAAA 696  
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QY 706 TGTAACAATAAGACATTCATGGATCAGGACCATGCACAAATGTGACACACAGTACATGT 765  
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Db 697 TGTAACGATAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTGACACACAGTACATGT 756  
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QY 766 ACACATGGAATTAGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 825  
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Db 757 ACACATGGAATTAGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 816  
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QY 826 GAAAGACATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACCATAATAGTACAG 885  
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Db 817 GAAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGATAAATGCTAAAAACCATCATAGTACAT 876  
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QY 886 CTAAATGAATCTGTAGTAATTAATTGTACAAGCCCAACAATAACAAGAAAGAGGTTA 945  
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Db 877 CTGAATGAATCTGTACAAAATTAATTGTACAAGCCCAACTACAATAAAAAGAAAAAGGATA 936  
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QY 946 TCTATAGGACCAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAA 1005  
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Db 937 CATATAGGACCAGGAGAGCATTTTATACAACAACAAAAATATAATAGGAACCTATAAGACAA 996  
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Db 997 GCACATTGTAACATTAGTAGAGCAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056  
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QY 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA 1125  
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Db 1057 TTAAAGAACAAATTTAAGAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116  
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QY 1126 GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATCTTCTACTGTAATACAGCACAA 1185  
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Db 1117 GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176  
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QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAAATGGCACTGAAGGAAATGAC 1242  
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Db 1177 CTGTTTAAATAGTACTTGGAAATGGTAATAATACTTGGAAATAATACTACAGGGTCAAATAAC 1236  
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QY 1243 ATAATCACACTCCAATGCAGAATAAAAACAAAATTAATAATATGTGGCAGAAAGTAGGAAAA 1302  
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Db 1237 AATATCACACTTCAATGCAGAAAATAAAACAAAATTATAAACATGTGGCAGGAAGTAGGAAAA 1296  
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QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAAATTAGATGTTTCAATCAAAATATTACAGGGCTG 1362  
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QY 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419  
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Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGGACACCAAGCACCGAGATCTTCAGACCT 1416  
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QY 1420 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGA 1479  
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Db 1417 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTAGTAACA 1476  
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QY 1480 ATTGAACCAATAGGAGTAGCACCACCCAGGGCAAGAGAAACAGTGCACAAAGAGAAAAA 1539  
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Db 1477 ATTGAACCAATTAGGAGTAGCACCACCCAGGCAAGGCAAGAGAAAGAGTGGTGCAGAGAGAAAAA 1536  
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QY 1540 AGACCGGATCCAAGA 1554  
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Db 1537 AGACGAGGATAGGA 1551  
|||||

RESULT 11

US-08-709-609-3  
; Sequence 3, Application US/08709609  
; Patent No. 5858775  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/709,609  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858775and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-709-609-3  
; Query Match 53.1%; Score 1172.2; DB 2; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 1.3e-276;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
QY 58 TCGGCTTCGAGATCCATGCTCCTCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117  
|||  
Db 40 TGGGATGGGGCACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99  
|||  
QY 118 TGGGTACAGTCTATTATATGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTTTGT 177  
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Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAAAAGCAACCACTCTATTTTGT 159  
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QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACATGCTGT 237  
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Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTGGGCCACACAGCCTGT 219  
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QY 238 GTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297  
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Db 220 GTACCCACAGACCCCAACCCACAAGAGTAGAATGGTAAATGTGACAGAAAAATTTAAC 279  
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QY 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357  
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QY 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATAATTG 417  
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QY 418 -----AATATCACTAAGAATACTACTAATCCCCTAGTAGCAGCTGGGGAATG 465  
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Db 460 ATAAAGGGAGGAGAAATGAAAAACTGCTCTTTCAATATCACCACNAGCATAGAATAAAG 519  
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QY 526 GTAAAGAAAGATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAAT 585  
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QY 646 GTATCCTTTTCAGCCCAATCCCATACATTATTGTGTCCCGCTGGGTTTGGATGCTAAAG 705  
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Db 637 ATATCCTTTTGAGCCCAATCCCATACACTATTGTGCCCCGGCTGGTTTTCGATTCTAAAA 696  
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QY 706 TGTAACAATAAGACATTTCAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAATGT 765  
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QY 886 CTAAATGAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTA 945  
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QY 946 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACAATAATAGGAGATATAAGACAA 1005  
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Db 937 CATATAGGACCGGAGAGCATTTTATACAACAACAAAAAATAATAATAGGAACCTATAAGACAA 996  
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Db	997	GCACATTGTAACATTAGTAGACGACAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA	1056
QY	1066	TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCA	1125
Db	1057	TTAAAAGAACAAATTTAAGAAATAAAA CAATAGTCTTTTAATCAATCCTCAGGAGGGGACCCA	1116
QY	1126	GAAATTGTAATGCACAGCTTTTAATTTGTGGAGGGGAATCTTCTACTGTAATACAGCACAA	1185
Db	1117	GAAATTGTAATGCACAGCTTTTAATTTGTGGAGGGGAATTTTCTACTGTAATACATCACCA	1176
QY	1186	CTGTTTAATAGTACTTTGGAATG--TTACTGGAGGGACAAAATGGCACTGAAGGAAATGAC	1242
Db	1177	CTGTTTAATAGTACTTTGGAATGGTAATAATACTTTGGAATAATACTACAGGGTCAAAATAAC	1236
QY	1243	ATAATCACACTCCCAATGCAGAAATAAAA CAAATTATAAATATGTGGCAGAAAGTAGGAAAA	1302
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QY	1303	GCAATGTATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTG	1362
Db	1297	GCAATGTATGCCCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTA	1356
QY	1363	CTACTAACAAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT	1419
Db	1357	CTATTAAACNAGAGATGGTGTAAAGGACACGACACGAAACGACCCGAGATCTTCAGACCT	1416
QY	1420	GGAGGAGGAGATATGAGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAAGA	1479
Db	1417	GGAGGAGGAGATATGAGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAACA	1476
QY	1480	ATTGAACCAATAGGATAGCACCCACCAGGGCAAAGACAGAAACAGTGC AAAGAGAAAAA	1539
Db	1477	ATTGAACCAATTAGGATAGCACCCCAACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAA	1536
QY	1540	AGACCGGATCCAAGA	1554
Db	1537	AGAGCAGCGATAGGA	1551

## RESULT 12

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US-09-552-950-3
; Sequence 3, Application US/09552950
; Patent No. 6541248
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/09/552,950
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus t
US-09-552-950-3

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Query Match	53.1%;	Score 1172.2;	DB 4;	Length 2571;
Best Local Similarity	87.9%;	Pred. No. 1.3e-276;		
Matches 1331; Conservative	0;	Mismatches 163;	Indels 21;	Gaps 4;

Qy	58	TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG	117
D <sub>b</sub>	40	TGGGGATGGGGCACGATGCTCCTTGGGTATTAAATGATCTGTAGTGCTACAGAAAAATTG	99
Qy	118	TGGGTACAGTCTATTATGGGTACTGTGTGGAGAGAAGCAACCACTCTATTTTGT	177
D <sub>b</sub>	100	TGGGTACAGTCTATTATGGGTACTGTGTGGAAAAGAAGCAACCACTCTATTTTGT	159
Qy	178	GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGGCCACACATGCCTGT	237



Db 1237 AATATCACACTTCAATGCAAAATAAAAAAATAATATAAATATGTCAGGAAAGTAGGAAAA 1296  
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCTCCCATGGAAGGACAAAATTAGATGTTTCATCAAAATATTACAGGCTA 1356  
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGGTGTAAAGCACCGGACACGAAACGACACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAAATTGGAGAAGTGAAATTATATAAATATAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAAATTGGAGAAGTGAAATTATATAAATATAAAGTAGTAACA 1476  
Qy 1480 ATTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAA 1539  
Db 1477 ATTGAACCATTAGGAGTAGCACCCACCAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAA 1536  
Qy 1540 AGACCGGATCCAAGA 1554  
Db 1537 AGACGCGATAGGA 1551

RESULT 13

US-09-936-572-3

; Sequence 3, Application US/09936572  
; Patent No. 6783981  
; GENERAL INFORMATION:  
; APPLICANT: UDEN, MARK  
; APPLICANT: MITROPHANOUS, KYRIACOS  
; TITLE OF INVENTION: ANTI-VIRAL VECTORS  
; FILE REFERENCE: 078883/0137  
; CURRENT APPLICATION NUMBER: US/09/936,572  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: PCT/GB00/01002  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: GB 9906177.2  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2571  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1

US-09-936-572-3

Query Match	53.1%;	Score 1172.2;	DB 4;	Length 2571;
Best Local Similarity	87.9%;	Pred. No. 1.3e-276;		
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Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117  
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Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTTTGT 177  
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACTCTATTTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAAGCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTTAAC 279  
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Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339  
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATAATTG 417  
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATGTTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
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Db 460 ATAAAGGAGGAGAAATGAAAAAATGCTCTCTTTCAATATCACCAAGCATAAAGATAAG 519  
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Db 520 ATGCAGAAAGAAATATGCACCTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT 576  
Qy 586 AATACTAAGTATAGGTTAAATAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAAG 645  
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAAAG 636  
Qy 646 GTATCCTTTTCAGCCCAATCCCATACATTATTGTGTCCCGGCTGGTTCGCGATGCTAAAAG 705  
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Qy 706 TGTAAACAATAAGACATTCAATGGATCAGGACCATGACAAAAATGTCAGCACAGTACAATGT 765  
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Qy 826 GAAGACATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAG 885  
Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGATAATGCTAAAAACCATCATAGTACAT 876  
Qy 886 CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTA 945  
Db 877 CTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAGAAAAAGGATA 936  
Qy 946 TCTATAGGACCAGGAGAGCAATTTTATGCAAGAAAGAAACAATAATAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACCAGGAGAGCAATTTTATACAACAACAAAAATAATAATAGGAACCTATAAGACAA 996  
Qy 1006 GCACATTTGTAACATTAGTAGACAAAAATGGAATAACACTTTAATCAATCCTCAGGAGGGACCCA 1065  
Db 997 GCACATTTGTAACATVAGTAGACAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056  
Qy 1066 TTAAGAGAAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA 1125  
Db 1057 TTAAGAAACAATTTAAGAAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116  
Qy 1126 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTGTAAATACAGCACAA 1185  
Db 1117 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176  
Qy 1186 CTGTTTAAATAGTACTTTGGAATG--TTACTGGAGGGACAAAATGGCACTGAAGGAAATGAC 1242  
Db 1177 CTGTTTAAATAGTACTTTGGAATGGTAATAATACTTTGGAATAATACTACAGGGTCAAATAAC 1236  
Qy 1243 AFAATCACACTCCAATGCAGAAATAAAAACAAAATTATAAATATGTTGGCAGAAAAGTAGGAAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAAACAAAATTATAAACAATGTTGGCAGGAAGTAGGAAAA 1296  
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356  
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGGTGTGAAGGACACCGGACACGAACCGACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAAATTGGAGAAAGTGAATTTATATAAATATAAAGTAGTAAGA 1479  
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QY 1420 GGAGGAGGAGATATGAGGACAATTTGGAGAAGTGAATTATATAATAATAAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGACAATTTGGAGAAGTGAATTATATAATAATAAAAGTAGTAACA 1476  
QY 1480 ATTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAAGAACAGTGCAAAGAGAAAAA 1539  
Db 1477 ATTGAACCAATTAGGAGTAGCACCCACCAGGCAAGGCAAGAGAAGAGTGGTGCAGAGAGAAAA 1536  
QY 1540 AGACCGGATCCAAGA 1554  
Db 1537 AGAGCAGCGATAGGA 1551

RESULT 15  
US-08-651-472-66/c  
; Sequence 66, Application US/08651472  
; Patent No. 6103244  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, Friedrich  
; APPLICANT: SCHEIFLINGER, Friedrich  
; APPLICANT: FALKNER, Falko Gunter  
; APPLICANT: PFLEIDERER, Michael  
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC  
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
; TITLE OF INVENTION: (HIV-1) ANTIGENS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/651,472  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/914,738  
; FILING DATE: 20-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/750,080  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6474 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid;  
; DESCRIPTION: Synthetic DNA oligonucleotide  
; IMMEDIATE SOURCE:  
; CLONE: pselp-gp160MN  
US-08-651-472-66

Query Match 53.1%; Score 1172.2; DB 3; Length 6474;  
Best Local Similarity 87.9%; Pred. No. 1.8e-276;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
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QY 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357  
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QY 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
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Db	2740	CTGTTTAATAGTACTTGGAAATGTTAATAATACTTGGATAATACTACAGGGTCAAATAAC	2681
Qy	1243	ATAATCACACTCCAATGCAGAATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAA	1302
Db	2680	AATATCACACTTCAATGCAAAATAAAACAAATTATAACATGTGGCAGGAAGTAGGAAAA	2621
Qy	1303	GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGCTG	1362
Db	2620	GCAATGTATGCCCTCCCATTGAAGGACAAATTAGATGTTTCATCAAATATTACAGGCTA	2561
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Perfect score: 2208  
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Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

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Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1222.2	55.4	9540	17 US-10-325-468-46	Sequence 46, Appl
2	1199.2	54.3	2612	15 US-10-414-692-20	Sequence 20, Appl
3	1197	54.2	1512	9 US-09-759-841-3	Sequence 3, Appli
4	1179.8	53.4	1422	18 US-10-728-195-7	Sequence 7, Appli
5	1174.2	53.2	3807	15 US-10-441-788-78	Sequence 78, Appl
6	1173	53.1	2552	10 US-09-966-931-27	Sequence 27, Appl
7	1173	53.1	2552	17 US-10-459-121-27	Sequence 27, Appl
8	1172.2	53.1	2571	9 US-09-999-183-3	Sequence 3, Appli
9	1172.2	53.1	2571	13 US-10-077-294-3	Sequence 3, Appli
10	1172.2	53.1	2571	13 US-10-163-886-3	Sequence 3, Appli
11	1172.2	53.1	2571	14 US-10-263-127-3	Sequence 3, Appli
12	1172.2	53.1	2571	15 US-10-375-777-3	Sequence 3, Appli

13	1172.2	53.1	2571	16 US-10-351-938-3	Sequence 3, Appli
14	1169.8	53.0	2573	10 US-09-966-931-29	Sequence 29, Appl
15	1169.8	53.0	2573	17 US-10-459-121-29	Sequence 29, Appl
16	1166.6	52.8	9704	17 US-10-325-468-40	Sequence 40, Appl
17	1166.4	52.8	9706	17 US-10-325-468-45	Sequence 45, Appl
18	1165.6	52.8	9715	17 US-10-325-468-44	Sequence 44, Appl
19	1165	52.8	9942	17 US-10-325-468-5	Sequence 5, Appli
20	1165	52.8	9942	17 US-10-325-468-54	Sequence 54, Appl
21	1164.2	52.7	2627	15 US-10-177-390-9	Sequence 9, Appli
22	1163.4	52.7	9942	17 US-10-325-468-1	Sequence 1, Appli
23	1163.4	52.7	9942	17 US-10-325-468-2	Sequence 2, Appli
24	1163.4	52.7	9942	17 US-10-325-468-7	Sequence 7, Appli
25	1163.4	52.7	9942	17 US-10-325-468-50	Sequence 50, Appl
26	1163.4	52.7	9942	17 US-10-325-468-51	Sequence 51, Appl
27	1163.4	52.7	9942	17 US-10-325-468-56	Sequence 56, Appl
28	1161.8	52.6	1932	15 US-10-387-336-31	Sequence 31, Appl
29	1161.8	52.6	2457	15 US-10-387-336-32	Sequence 32, Appl
30	1161.8	52.6	9942	17 US-10-325-468-3	Sequence 3, Appli
31	1161.8	52.6	9942	17 US-10-325-468-52	Sequence 52, Appl
32	1161.6	52.6	2570	10 US-09-966-931-31	Sequence 31, Appl
33	1161.6	52.6	2570	17 US-10-459-121-31	Sequence 31, Appl
34	1161	52.6	1419	15 US-10-387-336-30	Sequence 30, Appl
35	1160.8	52.6	9737	10 US-09-827-688-12	Sequence 12, Appl
36	1160.4	52.6	1929	14 US-10-032-162-12	Sequence 12, Appl
37	1160.2	52.5	9942	17 US-10-325-468-6	Sequence 6, Appli
38	1160.2	52.5	9942	17 US-10-325-468-55	Sequence 55, Appl
39	1160	52.5	1530	15 US-10-361-849-13	Sequence 13, Appl
40	1148.8	52.0	9181	18 US-10-475-024-14	Sequence 14, Appl
41	1148.8	52.0	9719	9 US-09-737-190A-1	Sequence 1, Appli
42	1148.8	52.0	9719	15 US-10-000-511A-1	Sequence 1, Appli
43	1148.8	52.0	9719	15 US-10-000-511A-2	Sequence 2, Appli
44	1148.8	52.0	9719	17 US-10-325-468-41	Sequence 41, Appl
45	1148.8	52.0	12425	15 US-10-000-511A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-325-468-46  
; Sequence 46, Application US/10325468  
; Publication No. US20040101823A1  
; GENERAL INFORMATION:  
; APPLICANT: Soong, Nay Wei  
; APPLICANT: Pekrun, Katja  
; APPLICANT: Shibata, Riri  
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL  
; FILE REFERENCE: 0166.210US  
; CURRENT APPLICATION NUMBER: US/10/325,468  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 9540  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus 1  
; FEATURE:  
; OTHER INFORMATION: parent JRCFSF DNA (GenBank Accession No. M38429)  
US-10-325-468-46

Query Match	55.4%	Score	1222.2;	DB	17;	Length	9540;
Best Local Similarity	90.0%;	Pred. No.	1.9e-271;				
Matches	1337;	Conservative	0;	Mismatches	133;	Indels	15; Gaps 2;
Qy	72	CATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGGGTACAGTCTA	131				
Db	6289	CTTGCTCCTTGGGACATTAATGATCTGTAGTGTCTAGAAAAAGTTGTGGGTACAGTCTA	6348				
Qy	132	TTATGGGGTACCTGTGTGAGAGAGCAACCACTCTATTTGTGCATCAGATGCTAA	191				



Db 6349 TTATGGGTACCTGTGTGGAAGAAACAACCACTCTATTTTGTGCATCAGATGCTAA 6408

Qy 192 AGCCTATGATACAGAGGTACATAATGTTTGGSCCACAACATGCTGTGTACCCACAGACCC 251

Db 6409 AGCATATGATACAGAGGTACATAATGTTTGGSCCACAACATGCTGTGTACCCACAGACCC 6468

Qy 252 CAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAATTTTAAACATGTGGHAAATAA 311

Db 6469 CAACCCACAAGAGTAGTATTGGGAAATGTAAACAGAAATTTTAAACATGTGGHAAATAA 6528

Qy 312 CATGGTAGATCAGATGCATGAGGATATAATCAAGTTTATGGGATGAAAGCCTAAAGCCATG 371

Db 6529 CATGGTAGAACAGATGCAGAGGATGTAATCAATTTATGGGATCAAAGCTTAAAGCCATG 6588

Qy 372 TGTAAAAATTAAACCCACTCTCTGTGTTACTTTTAAATTTGACATAATTTGAATATCACTAAGAA 431

Db 6589 TGTAAAAATTAAACCCACTCTCTGTGTTACTTTTAAATTTGCAAGATGT-----GAA 6636

Qy 432 TACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAGAAAAGGAGAAATAAAAAATTG 491

Db 6637 TGCTACTAATACCACCTAGTAGTAGTGAGGGAATGATGGAGAGAGGAGAAATAAAAAAATG 6696

Qy 492 CTCTTTCTATATCACCAACAGCATAAAGAAATAAGGTAAAGAAAAGAAATATGCACTTTTTAA 551

Db 6697 CTCTTTCAATATCACCAAAAGCATAAAGAGATAAGGTGCAGAAAGAAATATGCTCTTTTAA 6756

Qy 552 TAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTAATAAGTTG 611

Db 6757 TAAACTGGATGTAGTACCAATAGATAATAAGAAATAATACCAATAATAGTTAATAAGTTG 6816

Qy 612 TAACACCTCAGTCATTACAGAGCCTGTCCAAAGGTATCCTTTTTCAGCCAATTTCCATACA 671

Db 6817 TAACACCTCAGTCATTACAGAGCCTGTCCAAAGGTATCCTTTTGAACCAATTTCCCATACA 6876

Qy 672 TTATTGTGTCCCGGCTGGTTTTCGATGCTAAAGTGTAAACAATAAGACATTTCAATGGATC 731

Db 6877 TTATTGTGCCCCGGCTGGTTTTCGATTTCTAAAGTGTAAATAAAGACATTTCAATGGAAA 6936

Qy 732 AGGACCATGCACAAATGTACACAGATCAATGTACACATGGAATTAGGCCAGTGGTGC 791

Db 6937 AGGACAAATGTAAAAATGTACACAGTACAATGTACACATGGAATTAGGCCAGTAGTATC 6996

Qy 792 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAGACATAGTAATTAGATCTGAAAA 851

Db 6997 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAGAAAGTTGTAATTAGATCTGACAA 7056

Qy 852 TTTACAGACAAATGCTAAAACCATAAATAGTACAGCTAAATGAATCTGTAGTAATTAATTG 911

Db 7057 TTTTACGGACAATGCTAAAACCATAAATAGTACAGCTGAATGAATCTGTAAAAATTAATTG 7116

Qy 912 TACAAGACCCAAACAATAACAAGAAAGGTTATCTATAGGACCCAGGGAGAGCAATTTTA 971

Db 7117 TACAAGGCCCAGCAACAATAACAAGAAAAAGTATACATATAGGACCCAGGGAGAGCAATTTTA 7176

Qy 972 TGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTAGAGCAAA 1031

Db 7177 TACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTAGAGCACA 7236

Qy 1032 ATGGAATAACACTTTACAACAGATAGTTATAAAAAATTAAAGAAAAATTTAGGAATAAAAC 1091

Db 7237 ATGGAATAACACTTTAAAACAGATAGTTTGAAAAATTTAAGAGAACAAATTTAATAATAAAC 7296

Qy 1092 AATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTTTAATTG 1151

Db 7297 AATAGCTTTTACTCACTCCTCAGGAGGGGATCCAGAAATTTGTAATGCACAGTTTTAATTG 7356

Qy 1152 TGGAGGGGAATTTCTTCTACTGTAATAACAGCACTGTTTAAATAGTACTTTGGAATGTTAC 1211

Db 7357 TGGAGGGGAATTTTCTTACTGTAATTTCAACACAACTGTTTAAATAGTACTTTGGAATGATAC 7416

Qy 1212 TGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAAAACA 1271

Db 7417 TGAAGAGTCAAGTGGCACTGAAGGAAATGACACCATCATCACTCCATGCAGAAATAAAACA 7476

Qy 1272 AATTATAAATATGTGCAGAAAAGTAGGAAAAGCAATGTATGCCCCCTCCCATCACAGGACA 1331

Db 7477 AATTATAAACATGTGGCAGGAAGTGGGAAAAGCAATGTATGCTCCTCCCATTTAAAGGACA 7536

Qy 1332 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAAATAGTAC 1391

Db 7537 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTAA---AAA 7593

Qy 1392 TGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAATTTGGAGAAAG 1451

Db 7594 TGAGAGTGAGATCGAGATCTTCAGACCTGGAGGAGAGACATGAGGGACAATTTGGAGAAAG 7653

Qy 1452 TGAATTATATAATAATAAGTAGTAAGAATTGAAACCAATAGGAGTAGCACCCACCAAGGC 1511

Db 7654 TGAATTATATAATAATAAGTAGTAATAATTGAAACCATTAGGAGTAGCACCCACCAAGGC 7713

Qy 1512 AAAGAGAAAGACAGTGCAAAAGAGAAAAAGACCCGGATCCAAGAAAG 1556

Db 7714 AAAGAGAAAGAGTGGTGCAAGAGAAAAAGAGCGCAGTGGGAATAGG 7758

RESULT 2

US-10-414-692-20

; Sequence 20, Application US/10414692

; Publication No. US20030228607A1

; GENERAL INFORMATION:

; APPLICANT: X-Ceptor Therapeutics, Inc.

; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic

; TITLE OF INVENTION: profile

; FILE REFERENCE: 8012-002-US

; CURRENT APPLICATION NUMBER: US/10/414,692

; CURRENT FILING DATE: 2003-04-14

; PRIOR APPLICATION NUMBER: 60/372,650

; PRIOR FILING DATE: 2002-04-15

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20

; LENGTH: 2612

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-10-414-692-20

Query Match 54.3%; Score 1199.2; DB 15; Length 2612;

Best Local Similarity 90.2%; Pred. No. 2.2e-266;

Matches 1347; Conservative 0; Mismatches 123; Indels 24; Gaps 5;

Qy 66 GAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAAATTGTGGGTCAAC 125

Db 442 GGGCACCTTGCTCCTTGGGATATTAAATGATCTGTAGTCTGTAGAAAAAGTTGTGGGTCAAC 501

Qy 126 AGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTTTTGTGCATCAGA 185

Db 502 AGTCTATTATGGGTACCTGTGTGGAAAGAAAGCAACCACTCTATTTTTGTGCATCAGA 561

Qy 186 TGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGSCCACAACATGCCCTGTGTACCCAC 245

Db 562 TGCTAAAGCATATGATACAGAGGTACATAATGTTTGGSCCACAACATGCCCTGTGTACCCAC 621

Qy 246 AGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAA 305

Db 622 AGACCCCAACCCACAAGAAAGTAGTATTGGAAAAATGTAAACAGAACATTTTAACATGTGGAA 681

Qy 306 AAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAA 365

Db 682 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAA 741

Qy 366 GCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCACATAATTTGAATATCAC 425

Db 742 GCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCGAAGGATGT----- 792

Qy 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAA 485

Db	793	--GAATGCTACTAATACCACCTAAATGATAGCGAGGGAAACGATGGAGAGAGGAGAAATAAA	849
Qy	486	AAATTGCTCTTCTATATATCACCAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACT	545
Db	850	AAACTGCTCTTTCAATATATCACCAAGCATAAAGAGATGAGGTGCAGAAAGAATATGCTCT	909
Qy	546	TTTTAATAGACTTGTATGTAGTACCAATAGAAAATACTAAATAATACTAAGTATAGGTTAAT	605
Db	910	TTTTTATAAACCTTGTATGTAGTACCAATAG--ATAATAATAATACCAGCTATAGGTTGAT	966
Qy	606	AAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATTCC	665
Db	967	AAGTTGTACACCCTCAGTCATTACACAGGCCTGTCCAAAGATATCCTTTTGAGCCAATTCC	1026
Qy	666	CATACATTATTGTGCCGGCTGGGTTTGCATGCTAAAGTGTAAACAATAAGACATTCAA	725
Db	1027	CATACATTATTGTGCCGGCTGGTTCGCGATTCTAAAGTGTAAATGATAAGACGTTCAA	1086
Qy	726	TGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT	785
Db	1087	TGGAAAAGGACCATGTAAAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT	1146
Qy	786	GGTGTCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAACATAGTAATTAGATC	845
Db	1147	AGTATCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAACAGGTAGTAATTAGATC	1206
Qy	846	TGAAAAATTCACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT	905
Db	1207	TGACAAATTCACGAACAAATGCTAAAAACCATAATAGTACAGCTGAAAGAAATCTGTAGAAAT	1266
Qy	906	TAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGAGC	965
Db	1267	TAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGAGC	1326
Qy	966	ATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG	1025
Db	1327	ATTTTATCTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG	1386
Qy	1026	AGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTTAGGAA	1085
Db	1387	AGCAAAATGGAATGACACTTTAAAACAGATAGTTATAAAAAATTAAGAGAACAAATTTAGAA	1446
Qy	1086	TAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTT	1145
Db	1447	TAAAACAATAGCTTTAATCACTCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTT	1506
Qy	1146	TAATTGTGAGGGGAATTCTTCTACTGTAATACGCACAACTGTTTAATAGTACTTGG--	1203
Db	1507	TAATTGTGAGGAGAAATTTTCTACTGTAATTCACACAACCTGTTTAATAGTACTTGGAA	1566
Qy	1204	-AATGTTACTGGAGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGCAG	1262
Db	1567	TAATAATACTGAAGGTCAAAATAACACTGAAGGAAAT--ACTATCACACTCCCATGCAG	1623
Qy	1263	AATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCAT	1322
Db	1624	AATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCAT	1683
Qy	1323	CACAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACAGAGATGGAGG	1382
Db	1684	CAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTGCTATTAAACAAGAGATGGTGG	1743
Qy	1383	TAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGACAA	1442
Db	1744	--TATTAAATGAGAAATGGACCGAGATCTTCAGACCTGGAGGAGGAGATATGAGGACAA	1800
Qy	1443	TTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACC	1502
Db	1801	TTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATTAGGAGTAGCACC	1860
Qy	1503	CACCAGGGCAAAGAGAAGAACAGTGTCAAAGAGAAAAAGACCGGATCCAAGAAG	1556
Db	1861	CACCAAGGGCAAAGAGAAGAGTGGTGCAAGAGAAAAAGAGCAGTGGGAATAGG	1914

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RESULT 3
US-09-759-841-3
; Sequence 3, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus t
US-09-759-841-3

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Query Match 54.2%; Score 1197; DB 9; Length 1512;  
Best Local Similarity 89.2%; Pred. No. 5.6e-266;  
Matches 1316; Conservative 0; Mismatches 150; Indels 9; Gaps 2;

QY	74	TGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGCGGTACAGTCTATT	133
Db	38	TGCTGTGGAGCAGTCTCGTTTCGGCTAGCGTAGAAAAATTGTGGGTACAGTTTATT	97
QY	134	ATGGGGTACCTGTGTGGAGAGAAGCAACACCACCTCTATTTTGTGCATCAGATGCTAAAG	193
Db	98	ATGGGGTACCTGTGTGGAAAGAAGCAACACCACCTCTATTTTGTGCATCAGATGCTAAAG	157
QY	194	CCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCA	253
Db	158	CATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCA	217
QY	254	ACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGAAAAATAACA	313
Db	218	ACCCACAAGAGTAGAATTGGAAAAATGTGACAGAAAAATTTTAACATGTGAAAAATAACA	277
QY	314	TGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATGTG	373
Db	278	TGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTG	337
QY	374	TAAAAATTAAACCCCACTGTGTGTTACTTTTAAATTGCACTAAATTGA-----ATATCACTA	427
Db	338	TAAAAATTAACTCCACTCTGTGTTACTTTTAAATTGCACTGAATTTGAGGAATGCTACTAATG	397
QY	428	AGAACTACTATAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAATAAAA	487
Db	398	GGAATGACACTAATAACCACTAGTAGTAGCAGGGAAATGATGGGGGAGGAGAAAAATGAAA	457
QY	488	ATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGAAAAAGAAATATGCACTTT	547
Db	458	ATTGCTCTTTCAAAATCACCACAACACATAAGAGGTAAGGTGCAGAAAAAGAAATATGCACTTT	517
QY	548	TTAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACTAAAGTATAGGTTAATAA	607
Db	518	TTTATGAACCTTGTATATAGTACCAATAGATAATAATAGTAATAATAGTATAGGTTGATAA	577
QY	608	GTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATTCCCA	667
Db	578	GTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGATATCCTTTTGAGCCCAATTCCCA	637
QY	668	TACATTATTGTGTCCTGGCTGGGTTTTCGATGCTAAAGTGTAACAAATAAGACATTCAATG	727

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|||||
Db 638 TACATTATTGTGCCCCGGCTGGTTTTGGGATTCTTAAAGTGTAAAGATAAGAAGTTCAATG 697
|||||
QY 728 GATCAGGACCATTGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGG 787
|||||
Db 698 GAAAAGGACCATTGTTCAAATGTCAGCACAGTACAATGTACACATGGGATTAGGCCAGTAG 757
|||||
QY 788 TGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATCTG 847
|||||
Db 758 TATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCCG 817
|||||
QY 848 AAAATTTACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAATTA 907
|||||
Db 818 AAAATTTTCGGGACAATGCTAAAAACCATAATAGTACAGCTGAATGAATCTGTAGAAATTA 877
|||||
QY 908 ATTGTACAAGACCCCAACAATACAAGAAGAAGGTTATCTATAGGACCAGGGAGAGCAT 967
|||||
Db 878 ATTGTACAAGACCCCAACAATACAAGAAAAAGTATACATATAGGACCAGGCAGAGCAT 937
|||||
QY 968 TTTATGCAAGAAGAAAACATAATAGGAGATATAAGACAAGCACATTGTTAACATTAGTAGAG 1027
|||||
Db 938 TATATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTTAACCTTAGTAGAG 997
|||||
QY 1028 CAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAATA 1087
|||||
Db 998 CAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTAAGAGAACAAATTTGGGAATA 1057
|||||
QY 1088 AAACAAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTTGTAATGCACAGTTTTA 1147
|||||
Db 1058 AAACAAATAGTCTTTAAGCAATTCCTCAGGAGGGGACCCAGAAATTTGTACGCACAGTTTAA 1117
|||||
QY 1148 ATTGTGAGGGGAATTTCTTCTACTGTTAATACAGCACAACTGTTTAATAGTACTTGGAAATG 1207
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Db 1118 ATTGTGAGGGGAATTTTCTACTGTAAATTCACACAACTGTTTAATAGTACTTGGAAATG 1177
|||||
QY 1208 TTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1267
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Db 1178 TTACTGAAGAGTCAAATAACACTGTAGAAAAATAACAACAATCACACTCCCATGCAGAAATA 1237
|||||
QY 1268 AACAAATTATAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAG 1327
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Db 1238 AACAAATTATANAACATGTGGCAGAAAGTAGGAAGAGCAATGTATGCCCTCCCATCACAG 1297
|||||
QY 1328 GACAAATTAGATGTTTCATCAAATATTACAGGGCTGTACTAAACAAGAGATGGAGGTAATA 1387
|||||
Db 1298 GACAAATTAGATGTTTCATCAAATATTACAGGGCTGTCTATTAAACAAGAGATGGTGGTCCCG 1357
|||||
QY 1388 GTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAAATTGGA 1447
|||||
Db 1358 AGSCCAACA--AGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAAATTGGA 1414
|||||
QY 1448 GAACTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCA 1507
|||||
Db 1415 GAACTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCATTAGGAGTAGCACCCACCA 1474
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QY 1508 GGGCAAGAGAGAACAAGTGCNAAGAGAAAAAGA 1542
|||||
Db 1475 AGGCAAGAGAGAAGAGTGGTGCAGAGAGAAAAAAGA 1509
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RESULT 4
US-10-728-195-7
; Sequence 7, Application US/10728195
; Publication No. US20040191269A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Shan
; APPLICANT: Pal, Ranajit
; APPLICANT: Kalyanaraman, V.S.
; APPLICANT: Whitney, Stephen Charles
; APPLICANT: Keen, Tim
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS
; FILE REFERENCE: 07917-269001
```

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; CURRENT APPLICATION NUMBER: US/10/728,195
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/430,732
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-728-195-7

Query Match      53.4%; Score 1179.8; DB 18; Length 1422;
Best Local Similarity 90.4%; Pred. No. 5.1e-262;
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

QY 115 TTGTGGGTCACAGTCTATTATTTGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATT 174
Db 1 TTGTGGGTCACAGTCTATTATTTGGGGTACCTGTGTGAAAGAAGCAACCACCTCTATT 60

QY 175 TGTGCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACATGCC 234
Db 61 TGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCC 120

QY 235 TGTGTACCCACAGACCCCAACCCACAAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTT 294
Db 121 TGTGTACCCACAGACCCCAACCCACAAAGAAGTAGAATTGGAAAAATGTGACAGAAAAATTT 180

QY 295 AACATGTGGAAAAATTAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGAT 354
Db 181 AACATGTGGAAAAATTAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGAT 240

QY 355 GAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAAATTGCACATAAT 414
Db 241 CAAAGCCTAAAGCCATGTGTAAAAATTAACTCCACICTGTGTTACTTTAAAATTGCACATGAT 300

QY 415 TTGA-----ATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATG 468
Db 301 TTGAGGAATGCTACTAATGGGAATGACACTAATACCCTAGTAGTAGCAGGGAAATGATG 360

QY 469 GAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAGGTA 528
Db 361 GGGGAGGAGAAATGAAAAATTGCTCTTTCAAAATCACACAAAAACATAAGAGGTAAGGTG 420

QY 529 AAGAAAGAATATGCACITTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAAT 588
Db 421 CAGAAAGAATATGCACITTTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAAT 480

QY 589 ACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCAATTACACAGGCCCTGTCCAAAAGGTA 648
Db 481 AATAGATATAGGTTGATAAGTTGTAAACACCTCAGTCAATTACACAGGCCCTGTCCAAAAGTA 540

QY 649 TCCTTTCAGCCAATTCCCATACATTATTGTGTCCCGCTGGGTTTGGCATGCTAAAAGTGT 708
Db 541 TCCTTTGAGCCAATTCCTCATACATTATTGTGCCCGGCTGGTTTTCGGATTCTAAAAGTGT 600

QY 709 AACAAATAAGACATTCAATGGATCAGGACCATTGCACAAATGTGCAGCACAGTACAATGTACA 768
Db 601 AAAGATAAGAAGTTCAATGGAAAAAGGACCATTGTTCAAAATGTCAGCACAGTACAATGTACA 660

QY 769 CATGGAATTAGGCCAGTGGTGTCAAACCTCAAACCTGCTGTTAAATGGCAGTCTAGCAGAAGAA 828
Db 661 CATGGGATTAGGCCAGTAGTATCAACTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAA 720

QY 829 GACATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAGCTA 888
Db 721 GAGGTAGTAATTAGATCCGAAAAATTTTCGGGACAATGCTAAAAACCATAATAGTACAGCTG 780

QY 889 AATGAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAAATACAAGAAGAGTTTATCT 948
Db 781 AATGAATCTGTAGAAATTAATTGTACAAGACCCCAACAACAAATACAAGAAGAGTATACAT 840

QY 949 ATAGGACCAGGGAGAGCAATTTTATGCAAGAAGAAAACATAATAGGAGATATAAGACAAGCA 1008
```



|||||  
Db 841 ATAGGACAGGCAGAGCATTATATACAACAGGAGAAATAATAGGAGATATAAGACAAGCA 900  
Qy 1009 CATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTA 1068  
Db 901 CATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTA 960  
Qy 1069 AGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCAGAA 1128  
Db 961 AGAGAAACAATTTGGGAATAAAACAATAGTCTTTAAGCATTCCTCAGGAGGGGCCAGAA 1020  
Qy 1129 ATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAAC TG 1188  
Db 1021 ATTGTGACGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATTCACACAAC TG 1080  
Qy 1189 TTTAATAGTACTTGGAAATGTTACTGAGGGGACAAATGGCACTGAAGGAAATGACATAATC 1248  
Db 1081 TTTAATAGTACTTGGAAATGTTACTGAAGAGTCAAATAACACTGTAGAAAAATAACACAATC 1140  
Qy 1249 ACACCTCAATGCAGAAATAAAACAATTAATAAATATGTGGCAGAAAAGTAGGAAAAGCAATG 1308  
Db 1141 ACACCTCCCATGCAGAAATAAAACAATTAATAAATATGTGGCAGAAAAGTAGGAAAGCAATG 1200  
Qy 1309 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTA 1368  
Db 1201 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTA 1260  
Qy 1369 ACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTGAGACTCTTCAGACCTGGAGGAGGA 1428  
Db 1261 ACAAGAGATGGTGGTCCAGAGGCAACA ---AGACCGAGGTCTTCAGACCTGGAGGAGGA 1317  
Qy 1429 GATATGAGGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAAGAATTTGAACCA 1488  
Db 1318 GATATGAGGGACAATTTGGAGAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCA 1377  
Qy 1489 ATAGGAGTAGCACCCACCAGGCAAGGCAAGAGAAACAGAGTGCA 1529  
Db 1378 TTAGGAGTAGCACCCACCAGGCAAGGCAAGAGAGAGTGGTGGA 1418

RESULT 5  
US-10-441-788-78/c  
; Sequence 78, Application US/10441788  
; Publication No. US20030223987A1  
; GENERAL INFORMATION:  
; APPLICANT: Virogenetics Corporation  
; APPLICANT: Paolletti, Enzo  
; APPLICANT: Tartaglia, James  
; APPLICANT: Cox, William I  
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus  
; FILE REFERENCE: 454310-2690.1  
; CURRENT APPLICATION NUMBER: US/10/441,788  
; CURRENT FILING DATE: 2003-05-20  
; PRIOR APPLICATION NUMBER: US/09/136,159A  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: US 08/417,210  
; PRIOR FILING DATE: 1995-04-05  
; PRIOR APPLICATION NUMBER: US 08/223,842  
; PRIOR FILING DATE: 1994-04-06  
; PRIOR APPLICATION NUMBER: US 07/897,382  
; PRIOR FILING DATE: 1992-06-11  
; PRIOR APPLICATION NUMBER: US 07/715,921  
; PRIOR FILING DATE: 1991-06-14  
; PRIOR APPLICATION NUMBER: US 08/105,483  
; PRIOR FILING DATE: 1993-08-12  
; PRIOR APPLICATION NUMBER: US 07/847,951  
; PRIOR FILING DATE: 1992-03-06  
; PRIOR APPLICATION NUMBER: US 07/713,967  
; PRIOR FILING DATE: 1991-06-11  
; PRIOR APPLICATION NUMBER: US 07/666,056  
; PRIOR FILING DATE: 1991-03-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 78  
; LENGTH: 3807  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand  
US-10-441-788-78

Query Match 53.2%; Score 1174.2; DB 15; Length 3807;  
Best Local Similarity 88.1%; Pred. No. 1.6e-260;  
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

Qy 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111  
Db 1668 TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609  
Qy 112 AAATTGTGGGTACAGTCTTATTTATGGGTACCTGTGTGGAGAGAAGCAACCACCTCTA 171  
Db 1608 AAATTGTGGGTACAGTCTTATTTATGGGTACCTGTGTGGAAAGAAGCAACCACCTCTA 1549  
Qy 172 TTTTGTGCATCAGATGCTAAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231  
Db 1548 TTTTGTGCATCAGATGCTAAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489  
Qy 232 GCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAT 291  
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGAATGGTAAATGTGACAGAAAAT 1429  
Qy 292 TTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351  
Db 1428 TTAAACATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGG 1369  
Qy 352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCAC 411  
Db 1368 GATCAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCAC 1309  
Qy 412 AATTG-----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGG 459  
Db 1308 GATTGAGGAATACTACTAATACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGAG 1249  
Qy 460 GGAATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGA 519  
Db 1248 GGAACAATAAAGGAGGAGAAATGAAAAAATGCTCTTTCAATATCACCACAAGCATAGA 1189  
Qy 520 AATAAGGTAAAGAAAGATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAAT 579  
Db 1188 GATAAGATGCAGAAAGAAATATGCACCTCTTTATAAACTTGATATAGTATCAAT---AAAT 1132  
Qy 580 ACTAATAATACTAAGTATAGTTAATGAAGTTGTAAACACCTCAGTCATTACACAGGCCTGT 639  
Db 1131 AATGATAGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT 1072  
Qy 640 CCAAAGGTATCCTTTTCAGCCAATTTCCCATACATTTATGTGTCCCGCTGGTTTGCAGATG 699  
Db 1071 CCAAAGATATCCTTTTGAGCCAATTTCCCATACACTATTGTGCCCGCTGGTTTGCAGATT 1012  
Qy 700 CTAAAGTGTAACAATAAGACATTTCAATGGATCAGGACCATGCACAAAATGTCAGCACAGTA 759  
Db 1011 CTAAAGTGTAACCGATAAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAAATGTTCAGCACAGTA 952  
Qy 760 CAATGTACACATGGAAATTTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTA 819  
Db 951 CAATGTACACATGGAAATTTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA 892  
Qy 820 GCAGAAAGACATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATA 879  
Db 891 GCAGAAAGAGAGGTAGTAATTAGATCTGAGAAATTTCAATGATAATGCTAAAAACCATATA 832  
Qy 880 GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAGACCCCAACAATAACAAGAGA 939  
Db 831 GTACATCTGAATGAATCTGTACAAATTAATTGTACAGACCCCAACTACAATAAAAGAAA 772  
Qy 940 AGTTATCTATAGGACCAGGAGAGCATTTTATGCAAGAAAGAACATAATAGGAGATATA 999

Db 771 AGGATACATATAGGACCAGGAGAGCATTTTATACACAAAAATATAATAGGAACTATA 712  
Qy 1000 AGACAAGCACATTGTTAAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTT 1059  
Db 711 AGACAAGCACATTGTTAAACATTAGTAGAGCAAAAATGGAATGACACTTTAAGACAGATAGTT 652  
Qy 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGG 1119  
Db 651 AGCAAAATTAAGAAGAACAAATTTAAGAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGG 592  
Qy 1120 GACCCAGAAAATGTAATGCACAGTTTAAATTTGAGGGAATTTCTTACTGTAAATACA 1179  
Db 591 GACCCAGAAAATGTAATGCACAGTTTAAATTTGAGGGAATTTCTTACTGTAAATACA 532  
Qy 1180 GCACAACTGTTTAATAGTACTTGGAAATGTTACTGGAGGACAAAATGGCACTGAAG--A 1236  
Db 531 TCACCACTGTTTAATAGTACTTGGAAATGTTAAATAATACTTGGAAATAATACTACAGGTC 472  
Qy 1237 AATGACATAATCACACTCCCAATGCAGAAATAAAACAAAATTTATAAATATGTGGCAGAAAGTA 1296  
Db 471 AATAACAATATCACACTTCAATGCAAAATAAAACAAAATTTATAAACATGTGGCAGGAAGTA 412  
Qy 1297 GGAAGAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACA 1356  
Db 411 GGAAGAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAATATTACA 352  
Qy 1357 GGGCTGCTACTAACAAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTC 1413  
Db 351 GGGCTACTATTAAACAAGAGATGGTGAAGGACACCGGACAGCAACGACACCCGAGATCTTC 292  
Qy 1414 AGACCTGGAGGAGGAGATATGAGGACAAATTTGGAGAAGTGAATTTATATAAATATAAAGTA 1473  
Db 291 AGACCTGGAGGAGGAGATATGAGGACAAATTTGGAGAAGTGAATTTATATAAATATAAAGTA 232  
Qy 1474 GTAACAATTGAACCAATAGGATAGCACCCACCAGGGCCAAAGAGAACAAGTGCRAAGA 1533  
Db 231 GTAACAATTGAACCAATTAGGATAGCACCCACCAGGGCCAAAGAGAAGAGTGGTGCAGAGA 172  
Qy 1534 GAAAAAAGA 1542  
Db 171 GAAAAAAGA 163

RESULT 6  
US-09-966-931-27  
; Sequence 27, Application US/099666931  
; Publication NO. US20030064361A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
; STREET: 3 Embarcadero Center  
; City: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/966,931  
; FILING DATE: 27-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/492,739  
; FILING DATE: 2000-01-27  
; ATTORNEY/AGENT INFORMATION:

; NAME: Haliday, Emily  
; REGISTRATION NUMBER: 38903  
; REFERENCE/DOCKET NUMBER: 14918-704  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-393-2000  
; TELEFAX: 415-393-2286  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2552 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2552  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-966-931-27  
  
Query Match 53.1%; Score 1173; DB 10; Length 2552;  
Best Local Similarity 88.8%; Pred. No. 2.5e-260;  
Matches 1337; Conservative 0; Mismatches 135; Indels 33; Gaps 5;  
  
Qy 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC 123  
Db 46 TGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAGAAAAATTGTGGGTC 105  
  
Qy 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTTTGTGCATCA 183  
Db 106 ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACTCTATTTTGTGCATCA 165  
  
Qy 184 GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC 243  
Db 166 GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC 225  
  
Qy 244 ACAGACCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303  
Db 226 ACAGACCCCAACCCACAAGAAATAGGATTGGAAAAATGTAAACAGAAAAATTTTAAACATGTGG 285  
  
Qy 304 AAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363  
Db 286 AAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTTA 345  
  
Qy 364 AAGCCATGTGTAATAATTAAACCCCACTCTGTGTTACTTTAAATTCGACTAATTTGAATATC 423  
Db 346 AAGCCATGTGTAATAATTAAACCCCACTATGTGTTACTTTAAATTCGACTGATTG----- 399  
  
Qy 424 ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAATA 483  
Db 400 ---AAAAATGCTACTAATAACCACTAGTAGCAGCTGGGAAAGATGGAGAGAGGAGAAATA 456  
  
Qy 484 AAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAGAAAGAAATATGCA 543  
Db 457 AAAAACTGCTCTTTCAATGTCAACCAAGTATAAGAGATAAGATGAAGAAATGAATATGCA 516  
  
Qy 544 CTTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTA 603  
Db 517 CTTTTTATAAACTTGATGTAGTACCAATAG---ATAATGATAATACTAGCTATAGGTTG 573  
  
Qy 604 ATAAAGTTGTAACACCTCAGTCATTAACAGGCCCTGTCCAAGGTTATCCTTTCAGCCCAATT 663  
Db 574 ATAAAGTTGTAACACCTCAGTCATTAACAGGCCCTGTCCAAGGTTATCCTTTGAGCCCAATT 633  
  
Qy 664 CCCATACATTATTGTGTCCCGGCTGGGTTTTCGGATGCTTAAAGTGTAAACAATAAGACATTTC 723  
Db 634 CCCATACATTATTGTGTCCCGGCTGGTTCGGATTCCTTAAAGTGTAGAGATAAAAAGTTTC 693  
  
Qy 724 AATGGATCAGGACCATGCACAAATGTCAGCACAGTACATGATGATGATGATGATGATGATG 783  
Db 694 AACGGAACAGGACCATGTACAAATGTCAGCACAGTACATGATGATGATGATGATGATGATG 753  
  
Qy 784 GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA 843

Db	754	GTAGTATCAACTCAACTGCTGTTAAATGGCAGTTTAGCAGAAGAAGTAGTAATTAGA	813
QY	844	TCTGAAAAATTTTCACAGACAAATGCTAAAAACCATATAGTACAGCTAAATGAATCTGTAGTA	903
Db	814	TCTGCCAAATTTCTCGGACAAATGCTAAAAACCATATAGTACAGCTGAACGAATCTGTAGAA	873
QY	904	ATTAATTTGTACAAGACCCCAACAACAATACAAGAAAGGTTTATCTATAGGACCAGGGAGA	963
Db	874	ATTAATTTGTACAAGACCCCAACAACAATACAAGAAAGTATACATATAGGACCAGGGAGA	933
QY	964	GCATTTTATGCAAGAAGAAAACATATAGGAGATATAAAGACAAGCACATTGTAAACATTAGT	1023
Db	934	GCATTTTATGCAACAGGAGAAAATATAGGAGACATAAGACAAGCACATTGTAAACCTTAGT	993
QY	1024	AGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAAATTAAGAGAAAAATTTAGG	1083
Db	994	AGCACAAAATGGAATAATACTTTTAAACAGATAGTTACAAAATTAAGAGAACATTTT---	1050
QY	1084	AATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTTGAATGCACAGT	1143
Db	1051	AATAAAACAATAGTCTTTTAATCACTCCTCAGGAGGGGACCCAGAAAATTTGAATGCACAGT	1110
QY	1144	TTTAAATTTGTGGAGGGGAATTTCTTCTACTGTATAACAGCACAACTGTTTAAATAGTACTTGG	1203
Db	1111	TTTAAATTTGTGGAGGGGAATTTTCTACTGTATAACAACACCACTGTTTAAATAGTACTTGG	1170
QY	1204	AATGTTACTGGAGGGACAAAATGGCACTGAAGGAAATGA-----CATAAATCACA	1251
Db	1171	AATTATACTTATCTTGAATAATACTGAAGGGTCAAATGACACTGGAAGAAATATCACA	1230
QY	1252	CTCCAATGCAGATAAATAAATAAATAATGTGGCAGAAAAGTAGGAAAAGCAATGTAT	1311
Db	1231	CTCCNAATGCAGATAAATAAATAAATAATGTGGCAGGAAAGTAGGAAAAGCAATGTAT	1290
QY	1312	GCCCCTCCCATCAGAGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACA	1371
Db	1291	GCCCCTCCCATAGAGACAAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTAAACA	1350
QY	1372	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT	1431
Db	1351	AGAGATGGTGGTATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAGAT	1404
QY	1432	ATGAGGGACAAATTTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAAACCAATA	1491
Db	1405	ATGAGGGACAAATTTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAAACCAATA	1464
QY	1492	GGAGTAGCACCCACAGGGCAAAGAGAAAGAACAGTGCAAAAGAGAAAAAAGACCGGATCCA	1551
Db	1465	GGAGTAGCACCCACAGGGCAAAGAGAAAGAGTGTATGCAGAGAGAAAAAAGACGAGTGGGA	1524
QY	1552	AGAAG	1556
Db	1525	ATAGG	1529

## RESULT 7

US-10-459-121-27  
; Sequence 27, Application US/10459121  
; Publication No. US20040121317A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; Nakamura, Gerald R.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
; STREET: 3 Embarcadero Center  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
;





Db 757 ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 816  
Qy 826 GAAGACATAGTAATTAGATCTGAAAATTTACAGACAATGCTAAACCATAATAGTACAG 885  
Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTCACGTGATAATGCTAAAACCATCATAGTACAT 876  
Qy 886 CTAATGAATCTGTAGTAATTAAATTTGTACAAGACCCCAACAACATAACAAGAAGGTTA 945  
Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAAGACCCCAACTACAATAAAGAAAAGGATA 936  
Qy 946 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACATAATAAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACCGGAGAGCATTTTATACAACAAAATAATAAGAACTATAAGACAA 996  
Qy 1006 GCATTTGTAAACATTAGTAGAGCAAAATGGAATAACACTTTACAAACAGATAGTTATAAAA 1065  
Db 997 GCACATTTGAACATTAGTAGAGCAAAATGGAATGACACTTTAAGACACAGATAGTTAGCAAA 1056  
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA 1125  
Db 1057 TTAAGAGAACAAATTTAAGAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116  
Qy 1126 GAAATTTGTAATGCACAGTTTTTAATTTGTGAGGGGAATTTCTTACTGTATAACAGCAAA 1185  
Db 1117 GAAATTTGTAATGCACAGTTTTTAATTTGTGAGGGGAATTTTCTACTGTAATACATACCA 1176  
Qy 1186 CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGGACAATGGCAGTGAAGGAAATGAC 1242  
Db 1177 CTGTTTAATAGTACTTGGAAATGTTAATAATACTTGGAAATAATACTACAGGGTCAAAATAAC 1236  
Qy 1243 ATAATCACACTCCAAATGCAGAAATAAAACAAATTAATAATATGTGGCAGAAAAGTAGGAAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTAATAACATGTGGCAGGAAGTAGGAAAA 1296  
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356  
Qy 1363 CTAATAACAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTACAAGAGATGGTGGTGAAGACACGGACACGACACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTTATATAATAATAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTTATATAATAATAAGTAGTAACA 1476  
Qy 1480 ATTGAACCAATAGGAGTAGCACCCACCGGGCAAAGAGAGAACAGTGCAAAGAGAAAAA 1539  
Db 1477 ATTGAACCAATAGGAGTAGCACCCACCAAGGCNAAGAGAAGAGTGGTGCAGAGAGAAAAA 1536  
Qy 1540 AGACCGGATCCAAGA 1554  
Db 1537 AGAGCAGCGATAGGA 1551

RESULT 9

US-10-077-294-3  
; Sequence 3, Application US/10077294  
; Publication No. US20020159979A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; City: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/077,294  
; FILING DATE: 15-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/691,604  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020159979Aland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-077-294-3

Query Match 53.1%; Score 1172.2; DB 13; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 3.8e-260;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTG 117  
Db 40 TGGGATGGGCACGATGCTCCTTTGGGTTATTAATGATCTGTAGTCTACAGAAAAATTG 99  
Qy 118 TGGGTCACAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCACCACCTCTATTTTGT 177  
Db 100 TGGGTCACAGTCTATTATGGGTACCTGTGTGGAGAAGCAACCACCACCTCTATTTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAAGAGTAGAATTTGGTAAATGTGACAGAAAAATTTAAC 279  
Qy 298 ATGTGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTTATGGGATGAA 357  
Db 280 ATGTGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTTATGGGATCAA 339  
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTG 417  
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTCGACTGATTG 399  
Qy 418 -----AATATCACTAAGAATACTACTAATCCCACCTAGTAGCAGCTGGGGAATG 465  
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAAATAGCGAGGAACA 459  
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACCAAGCATAGAAAAAAG 525  
Db 460 ATAAAGGAGGAGAAATGAAAAAACTGCTCTTTCAATATCACCACCAAGCATAGAGATAAG 519  
Qy 526 GTAAAGAAAGAAATATGCACTTTTTTAATAGACTTTGATGTAGTACCATAGAAAAATACTAAT 585  
Db 520 ATGCAGAAAGAAATATGCACTTCTTTATAAACTTGATATAGTATCAATAG---ATAATGAT 576  
Qy 586 AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAAG 645  
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAAAG 636  
Qy 646 GTATCCTTTTCAGCCCAATTTCCCATACATTATTGTGTCCCGCTGGGTTTCCGATGCTAAAAG 705

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Db      ||||| ATATCCTTTGAGCCAATTCCCATACACTATTGTGCCCGGCTGTTTTCGGATCTTAAAA 696
Qy      ||||| TGTAAACAATAAGACATTCAATGGATCAGGACCATGCAAAATGTCAGCACAGTACAATGT 765
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Qy      ||||| GAAACATAGTAATTAGATCTGAAAAATTTTCACAGACAAATGCTAAAAACCATAATAGTACAG 885
Db      ||||| GAAAGGTAGTAATTAGATCTGAGAAATTTCACTGATAATGCTAAACCATCATAGTACAT 876
Qy      ||||| CTAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAATAACAAGAAAGGTTA 945
Db      ||||| CTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAGAAAAAGGATA 936
Qy      ||||| TCTATAGGACCAAGGAGAGCAATTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAA 1005
Db      ||||| CATATAGGACCAAGGAGAGCAATTTATATACAACAAAAATATAATAGGAACTATAAGACAA 996
Qy      ||||| GCACATTGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTCAACAGATAGTTATAAAA 1065
Db      ||||| GCACATTGTAACATTAGTAGAGCAAAAATGGAATGACACTTTAAAGACAGATAGTTAGCAAA 1056
Qy      ||||| TTAAGAGAAAAATTTAGGAAATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGACCCA 1125
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Qy      ||||| CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGGCAAAATGGCACTGAAGGAATGAC 1242
Db      ||||| CTGTTTAATAGTACTTGGAAATGTTGTAATAATACTTGGAAATAATACTACAGGGTCAAATAAC 1236
Qy      ||||| ATAATCACACTCCAATGCAGAAATAAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAA 1302
Db      ||||| AATATCACACTTCAATGCAAAATAAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAA 1296
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Qy      ||||| GGAGGAGGAGATATGAGGGACAAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGA 1479
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Qy      ||||| ATTGAACCAATAGGAGTAGCACCCAGGGCAAAGAGAGAAACAGTGCAAAGAGAAAAA 1539
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US-10-163-886-3
; Sequence 3, Application US/10163886
; Publication No. US20020187129A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; Methods
; NUMBER OF SEQUENCES: 3
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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020187129Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-163-886-3
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Query Match      53.1%; Score 1172.2; DB 13; Length 2571;
Best Local Similarity 87.9%; Pred. No. 3.8e-260;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

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Db 937 CATATAGGACCGGAGAGCAFTTTATACAACAAAAAATATAATAGGAACTATAAGACAA 996  
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QY 1540 AGACCGGATCCAAGA 1554  
Db 1537 AGAGCAGCGATAGGA 1551  
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US-10-375-777-3  
; Sequence 3, Application US/10375777  
; Publication No. US20030147912A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/375,777  
; FILING DATE: 26-Feb-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/163,886  
; FILING DATE: 04-Jun-2002  
; APPLICATION NUMBER: 09/292,703  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20030147912A1and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-375-777-3  
Query Match 53.1%; Score 1172.2; DB 15; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 3.8e-260;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
QY 58 TGGCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117  
Db 40 TGGGATGGGCACGATGCTCTTGGTTATTAAATGATCTGTAGTGTCTACAGAAAAATTG 99  
QY 118 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGCAACACCACCTCTATTTTGT 177  
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Qy 1540 AGACCGGATCCAAGA 1554

Db 1537 AGAGCAGCGATAGGA 1551

RESULT 13

US-10-351-938-3

; Sequence 3, Application US/10351938

; Publication No. US20040009603A1

; GENERAL INFORMATION:

; APPLICANT: Oxford Biomedica (UK) Limited

; TITLE OF INVENTION: Anti-Viral Vectors

; FILE REFERENCE: 674524-2004

; CURRENT APPLICATION NUMBER: US/10/351,938

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: US/09/552,950

; PRIOR FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2571

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-10-351-938-3

Query Match 53.1%; Score 1172.2; DB 16; Length 2571;

Best Local Similarity 87.9%; Pred. No. 3.8e-260;

Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117

Db 40 TGGGGATGGGCACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGTACAGAAAAATTG 99

Qy 118 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTTTGT 177

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QY 1126 GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTACTGTAATACAGCACAA 1185

Db 1117 GAAATTGTAAATGCACAGTTTTTAATTGTAGAGGGGAATTTTTCTACTGTAAATACACACAA 1176  
QY 1186 CTGTTTTAATAGTACTTGGAAATGTTTACTGGAGGGACAAAATG-----GCACGAAAGGAAAT 1239  
Db 1177 TTGTTTGACAGTACTTGGGATAATACTATAAAGTGTCAAAATGGCACTAGCAGTGAAGAGAAT 1236  
QY 1240 GACATAATCACACTCCCAATGCAGAAATAAAACAATAATATAAAATATGTGGCAGAAAGTAGGA 1299  
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Db 1297 AAAGCAATGTATGCCCTCCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGG 1356  
QY 1360 CTGCTACTAACAAAGAGATGGAGGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 TTGCTATTAAACAAGAGATGGAGG-----TAGTAAACAACAGCATGAATGAGACCTTCAGACCT 1413  
QY 1420 GGAGGAGGAGATATGAGGGACAAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGA 1479  
Db 1414 GGAGGAGGAGATATGAGGGACAAATTGGAGAAAGTGAATTATACAAATATAAAGTAGTAAAA 1473  
QY 1480 ATTGAACCAATAGGAGTAGCACCCACCAGGCCAAAGAGAAACAGTGCAAAAGAGAAAAA 1539  
Db 1474 ATTGAACCAATTAGGAGTAGCACCCACCACCAAGGCAAGAGAAAGAGTGGTGCAGAGAGAAAA 1533  
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Db 1534 AGAGCAGTGGGAATAGG 1550

Search completed: November 12, 2004, 19:50:33  
Job time : 774.964 secs





Db 138 TCATAGAAGGCTGGACAGATAGAAGATGAAAAGGAFTCTTTCATGAAGATTTTGTATTTCAT 197

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Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGCGCACATGT 377

QY 1788 CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1847

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QY 1908 AGGACTCTATTATATCTATGSCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 1967

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QY 1968 AGCTCCATTATAGCCAGCCTTCGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 2027

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QY 2028 CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTTCGGGGCAACAATCCATTCTGGG 2087

Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTTCGGGGCAACAATCCATTCTGGG 677

QY 2088 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAGCCA 2147

Db 678 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAGCCA 737

QY 2148 AGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 2193

Db 738 AGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 783

RESULT 2

AY416062

LOCUS

DEFINITION

AY416062

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AY416062 786 bp DNA linear GSS 17-DEC-2003

Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY416062 GI:39772022

GSS.

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 786)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 786)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

FEATURES

source

gene

ORIGIN

Query Match 29.0%; Score 641.2; DB 9; Length 786;

Best Local Similarity 99.5%; Pred. No. 1.5e-146;

Matches 643; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1548 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 1607

Db 138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 197

QY 1608 GAAACCGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACCTGTGAGGA 1667

Db 198 GAAACCGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACCTGCGAGGA 257

QY 1668 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAAGAGGAGACGAA 1727

Db 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAAGAGGAGACGAA 317

QY 1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 1787

Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 377

QY 1788 CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1847

Db 378 CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 437

QY 1848 CACCATGAGCAACAACTTGTGTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 1907

Db 438 CACCATGAGCAACAACTTGTGTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497

QY 1908 AGGACTCTATTATATCTATGSCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 1967

Db 498 AGGACTCTATTATATCTATGSCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 557

QY 1968 AGCTCCATTATAGCCAGCCTTCGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 2027

Db 558 AGCTCCATTATAGCCAGCCTTCGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 617

QY 2028 CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTTCGGGGCAACAATCCATTCTGGG 2087

Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTTCGGGGCAACAATCCATTCTGGG 677

QY 2088 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAGCCA 2147

Db 678 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAGCCA 737

QY 2148 AGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 2193

Db 738 AGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 783

RESULT 3

CD638712

LOCUS

DEFINITION

ACCESSION

CD638712

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

CD638712 767 bp mRNA linear EST 17-JUN-2003

AGENCOURT 14532410 NIH MGC 191 Homo sapiens cDNA clone

IMAGE:30416146 5', mRNA sequence.

CD638712

CD638712.1 GI:31804800

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM215 row: h column: 11  
High quality sequence stop: 564.  
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/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

FEATURES  
source  
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/organism="Homo sapiens"  
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/tissue\_type="Pooled"  
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/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 25.8%; Score 570; DB 6; Length 767;  
Best Local Similarity 97.8%; Pred. No. 5e-129;  
Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
1548 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1607  
||  
27 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 86  
1608 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 1667  
||  
87 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 146  
1668 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTATAATCTTAAACAAAGAGGAGCGAA 1727  
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1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAATTCGCGCACATGT 1787  
||  
207 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAATTCGCGCACATGT 266  
1788 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 1847  
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267 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 326  
1848 CACCATGAGCAACAACTTGGTTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 1907  
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327 CACCATGAGCAACAACTTGGTTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 386  
1908 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 1967  
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387 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 446

QY 1968 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCTTACT 2027  
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Db 447 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCTTACT 506  
2028 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 2087  
||  
Db 507 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 566  
2088 AGGAGTATTTGAATTGCAACACAGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAGCCA 2147  
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Db 567 AGGAGTATTTGAATTGCAACACAGTGCTTCGGTGTGTTGTC-ATGTGACTGATCCNAGCNA 625

RESULT 4  
CD521613 806 bp mRNA linear EST 06-JUN-2003  
LOCUS AGENCOURT\_14356206 NIH\_MGC\_191 Homo sapiens cDNA clone  
DEFINITION IMAGE:30413128 5', mRNA sequence.  
ACCESSION CD521613  
VERSION CD521613.1 GI:31453331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 806)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM207 row: j column: 17  
High quality sequence stop: 466.  
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/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 22.9%; Score 505; DB 6; Length 806;  
Best Local Similarity 96.7%; Pred. No. 5e-113;  
Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;  
1548 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1607  
||



Db 232 TCATAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTCATGAAGATTTTGTATTTCAT 291

QY 1608 GAAAACGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGA 1667  
|||||

Db 292 GAAAACGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGA 351

QY 1668 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTAAACAAAGAGGAGACGAA 1727  
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Db 352 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTAAACAAAGAGGAGACGAA 411

QY 1728 GAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAATTCGGGCAATGT 1787  
|||||

Db 412 GAAAGANAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCANATTCGGGCAATGT 471

QY 1788 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1847  
|||||

Db 472 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 531

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Db 532 CACCATGAGCAACAACCTTGTTAAACCCTGGAAAATGGGAAACAGCTGACCGTTAAAAGACA 591

QY 1908 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 1967  
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Db 592 AAGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 651

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Db 652 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 711

QY 2028 CAGAGCTGCAAATACCCACAGTTCGGCCCAAACCTT-GCGGGCAACAATCCATTCACTTGG 2086  
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Db 712 CAGAGCTGCAAATACCCCCAGTTCGGCCCAACCTTGGCGGGCAAAACATCCCTTCCCTTG 771

QY 2087 GAG 2089

Db 772 GGG 774

RESULT 5

AY416063

LOCUS

DEFINITION

AY416063

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AY416063

Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY416063.1 GI:39772023

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 783)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 783)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

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/gene="TNFSF5"

/locus\_tag="HCM5765"

ORIGIN

Query Match 20.4%; Score 450.8; DB 9; Length 783;

Best Local Similarity 82.2%; Pred. No. 1.1e-99;

Matches 531; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

QY 1548 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1607  
|||

Db 138 TCATAGAAGATTGGATAAAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTTCAT 197

QY 1608 GAAAACGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGA 1667  
|||||

Db 198 AAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCCTTGTGAACTGTGAGGA 257

QY 1668 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATAATGTTAAACAAAGAGGAGACGAA 1727  
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Db 258 GATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAAGA---GAA 314

QY 1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 1787  
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Db 315 AAAAGAAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAAATTCGAGCACAGT 374

QY 1788 CATAAAGTGAGGCCAGCAGTFAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 1847  
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Db 375 TGTAAGCGAAGCCACAGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGGATATTA 434

QY 1848 CACCATGAGCAACAACCTTGGTTAACCCCTGGAAAAATGGGAAAACAGCTGACCGTTAAAAGACA 1907  
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Db 435 TACCATGAAAAGCAACTTGGTAATGCTTGAAAAATGGGAAAACAGCTGACCGTTAAAAGAGA 494

QY 1908 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 1967  
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Db 675 CGGAGTGTTTGAAATTACAAGCTGGTGTCTTCTGTGTTGTCAACGTCAGTGAAGCAAGCCA 734

QY 2148 AGTGAGCCATGGCACTGGCTTCACGTCCTTTTGGCTTACTCAAACCTC 2193  
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Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACCTC 780

RESULT 6

CD640741

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CD640741

AGENCOURT\_14542170 NIH MGC\_191 Homo sapiens cDNA clone

IMAGE:30414715 5', mRNA sequence.

CD640741

CD640741.1 GI:31808911

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 702)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.



Db	393	GAAGAAGAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT	452
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QY	1848	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	1907
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Db	573	AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTGTCCA	613
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DEFINITION	AGENCOURT 14355767 NIH_MGC_191 Homo sapiens cDNA clone		
	IMAGE:30412573 5', mRNA sequence.		
ACCESSION	CD520208		
VERSION	CD520208.1 GI:31451926		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 796)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Narayan Bhat cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDCM206 row: c column: 14 High quality sequence stop: 541.		
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	/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
ORIGIN			
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	Best Local Similarity	98.3%;	Pred. No. 1.7e-84;
	Matches 403; Conservative	0;	Mismatches 6; Indels 1; Gaps 1;

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Db	325	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	384
QY	1728	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGCGCACATGT	1787
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QY	1848	CACCATGAGCAACAACCTTGTTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	1907
Db	505	CACCATGAGCAACAACCTTGTTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	564
QY	1908	AGGACTCTATTATATCTATGCCCAAGTCA-CCTTCTGTTCCAAATCGGGAA	1956
Db	565	AGGACTCTATTATATCTATGCCCAAGTCACCCCTTCTGTTCCAAATTCGGGA	614
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LOCUS			
DEFINITION			
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sequence.			
CN794193			
CN794193.1 GI:47690173			
EST.			
SOURCE			
Bos taurus (cow)			
ORGANISM			
Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
Bovinae; Bos.			
REFERENCE			
1 (bases 1 to 571)			
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and			
Matukumalli,L.K.			
AUTHORS			
Construction and Analysis of a cDNA Library Generated From			
Intestinal Muscle and Epithelial Tissues of Holstein Cattle			
Unpublished (2004)			
JOURNAL			
Contact: Richard G. Baumann			
COMMENT			
Bovine Functional Genomics Lab			
ANRI			
BLDG 162; BARC-EAST, Beltsville, MD 20705, USA			
Tel: 3015048604			
Fax: 3015048744			
Email: rbaumann@anri.barc.usda.gov			
Single pass sequencing. Bases called and trimmed with phred			
0.000925 using options -trim_alt '' -trim_fasta. Vector identified			
by cross match using options -minmatch 12 -minscore 18			
Plate: 50 row: H column: 03			
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FEATURES			
source			













GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 5828.61 Seconds  
(without alignments)  
16453.933 Million cell updates/sec

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Perfect score: 2028  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1471	72.5	10000	14	AF038398	AF038398 Simian-Hu
2	1453.4	71.7	2046	6	CQ753919	CQ753919 Sequence
3	1453.4	71.7	2610	6	CQ753921	CQ753921 Sequence
4	1453.4	71.7	9860	14	AF217181	AF217181 Simian-Hu
5	1453.4	71.7	9860	14	SI089134	U89134 Simian-Huma
6	1453.4	71.7	10501	6	BD161892	BD161892 Nonhuman
7	1447.6	71.4	9713	14	HIV1U39362	U39362 Human immun
8	1339.4	66.0	2010	6	CQ753923	CQ753923 Sequence
9	1339.4	66.0	2574	6	CQ753925	CQ753925 Sequence
10	1262.8	62.3	2553	14	AY247221	AY247221 HIV-1 iso
11	1242.2	61.3	2568	14	AY426111	AY426111 HIV-1 clo
12	1240.6	61.2	2568	14	AY426112	AY426112 HIV-1 clo
13	1239	61.1	2568	14	AY426118	AY426118 HIV-1 clo
14	1237.4	61.0	2568	14	AY426110	AY426110 HIV-1 iso
15	1237.4	61.0	2568	14	AY426113	AY426113 HIV-1 clo
16	1237.4	61.0	2568	14	AY426115	AY426115 HIV-1 clo
17	1237.4	61.0	2568	14	AY426117	AY426117 HIV-1 clo
18	1235.8	60.9	2568	14	AY426114	AY426114 HIV-1 clo
19	1235.8	60.9	2568	14	AY426116	AY426116 HIV-1 clo

20	1227	60.5	3061	14	HIVENVBALA	M63929 Human immun
21	1225.4	60.4	3807	6	AR034235	AR034235 Sequence
22	1225.4	60.4	3807	6	I12144	I12144 Sequence 5
23	1225.4	60.4	3807	6	I28919	I28919 Sequence 5
24	1225.4	60.4	3808	14	HIVBAL1A	M68893 Human immun
25	1224.2	60.4	2559	14	AY669732	AY669732 HIV-1 iso
26	1223.4	60.3	2547	14	AY426125	AY426125 HIV-1 iso
27	1223.4	60.3	2547	14	AY426127	AY426127 HIV-1 clo
28	1221.8	60.2	2544	14	AY669726	AY669726 HIV-1 iso
29	1221.8	60.2	2547	14	AY426126	AY426126 HIV-1 clo
30	1221.8	60.2	9540	14	HIVJRCSP	M38429 Human immun
31	1220.8	60.2	2568	14	AY247225	AY247225 HIV-1 iso
32	1218.6	60.1	3211	14	HIVU45960	U45960 Human immun
33	1209	59.6	2552	6	I05789	I05789 Sequence 8
34	1208.2	59.6	2559	14	AF025750	AF025750 HIV-1 iso
35	1206.8	59.5	2577	14	AF025763	AF025763 HIV-1 iso
36	1201.2	59.2	3600	14	HIVBRVA	M21098 Human immun
37	1198.8	59.1	8896	14	HIVU63632	U63632 HIV-1 isola
38	1197	59.0	1512	6	AX153805	AX153805 Sequence
39	1197	59.0	1512	6	BD017695	BD017695 Assay met
40	1196	59.0	2565	14	AF025754	AF025754 HIV-1 iso
41	1195.4	58.9	2571	14	HIVENVB	L08656 Human immun
42	1195.4	58.9	9074	14	HIVU43096	U43096 Human immun
43	1195.2	58.9	2553	14	HIV1MB314	Y13719 Human immun
44	1195.2	58.9	2559	14	HIV1U36877	U36877 Human immun
45	1194.6	58.9	2559	14	AY247220	AY247220 HIV-1 iso

ALIGNMENTS

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LOCUS	AF038398	AF038398.1	GI:2828036				
DEFINITION	AF038398	AF038398.1	GI:2828036				
ACCESSION	AF038398	AF038398.1	GI:2828036				
VERSION	AF038398	AF038398.1	GI:2828036				
KEYWORDS	AF038398	AF038398.1	GI:2828036				
SOURCE	AF038398	AF038398.1	GI:2828036				
ORGANISM	AF038398	AF038398.1	GI:2828036				
REFERENCE	AF038398	AF038398.1	GI:2828036				
AUTHORS	AF038398	AF038398.1	GI:2828036				
TITLE	AF038398	AF038398.1	GI:2828036				
JOURNAL	AF038398	AF038398.1	GI:2828036				
MEDLINE	AF038398	AF038398.1	GI:2828036				
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AUTHORS	AF038398	AF038398.1	GI:2828036				
TITLE	AF038398	AF038398.1	GI:2828036				
JOURNAL	AF038398	AF038398.1	GI:2828036				
FEATURES	AF038398	AF038398.1	GI:2828036				
source	AF038398	AF038398.1	GI:2828036				
LTR	AF038398	AF038398.1	GI:2828036				
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Qy	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACAT	231		
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DEFINITION		CQ753919			
ACCESSION		CQ753919			
VERSION		CQ753919.1		GI:44845220	
KEYWORDS		Human immunodeficiency virus 1 (HIV-1)			
SOURCE		Human immunodeficiency virus 1			
ORGANISM		Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate			
REFERENCE		1			
AUTHORS		Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.			
TITLE		Recombinant measles viruses expressing epitopes of antigens of rna			
JOURNAL		viruses - use for the preparation of vaccine compositions			
FEATURES		Patent: WO 2004001051-A 24 31-DEC-2003;			
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Db 97 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACTCTA 156

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACAT 231

Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACAT 216

Qy 232 GCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAAT 291

Db 217 GCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAAT 276

Qy 292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351

Db 277 TTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336

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Db 337 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCAC 396

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RESULT 3

CQ753921

LOCUS CQ753921 2610 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 26 from Patent WO2004001051.

ACCESSION CQ753921

VERSION CQ753921.1 GI:44845221

KEYWORDS .

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

REFERENCE 1

AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.

TITLE Recombinant measles viruses expressing epitopes of antigens of rna

JOURNAL viruses - use for the preparation of vaccine compositions

Patent: WO 2004001051-A 26 31-DEC-2003;

INSTITUT PASTEUR (FR)

FEATURES

source Location/Qualifiers

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Best Local Similarity 98.3%; Pred. No. 2.6e-292;

Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Best Local Similarity 98.3%; Pred. No. 2.1e-292;
Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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RESULT 5

SIU89134

LOCUS

DEFINITION

Simian-Human immunodeficiency virus strain SHIV-89.6P, complete genome.

ACCESSION

U89134

VERSION

U89134.1 GI:2108163

KEYWORDS

SOURCE

ORGANISM

Simian-Human immunodeficiency virus

Simian-Human immunodeficiency virus

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE

1 (bases 1 to 9860)

AUTHORS

Karlsson,G.B., Halloran,M., Li,J., Park,I.W., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J. Characterization of molecularly cloned simian-human immunodeficiency viruses causing rapid CD4+ lymphocyte depletion in rhesus monkeys

TITLE

J. Virol. 71 (6), 4218-4225 (1997)

JOURNAL

MEDLINE

PUBMED

97296224

9151808

REFERENCE

2 (bases 1 to 9860)

AUTHORS

Karlsson,G.B., Halloran,M., Li,J., Park,I., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J. Direct Submission

TITLE

Submitted (10-FEB-1997) Human Retrovirology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA

JOURNAL

INSTITUTE

Location/Qualifiers

FEATURES

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Db	6735	AATTTGAATATCACTAAGAATACTACTAATAATCCCACTAGTAGCAGCTGGGAATGATGGAG	6794	
Qy	472	AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG	531	
Db	6795	GAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG	6854	
Qy	532	AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACT	591	
Db	6855	AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACT	6914	
Qy	592	AAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTAACAGGCCTGTCCAAAGGTATCC	651	
Db	6915	AAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTAACAGGCCTGTCCAAAGGTATCC	6974	
Qy	652	TTTCAGCCCAATTCCCATACATTATTGTGTCCCGGTGGGTTTCGATGCTAAAGTGAAC	711	
Db	6975	TTTCAGCCCAATTCCCATACATTATTGTGTCCCGGTGGGTTTCGATGCTAAAGTGAAC	7034	
Qy	712	AATAAGACATTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACAT	771	
Db	7035	AATAAGACATTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACAT	7094	
Qy	772	GGAATTAGGCCAGTGGTGCTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAC	831	
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Qy	832	ATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATAATAGTACAGCTAAAT	891	
Db	7155	ATAGTAATTAGATCTGAAGATTTTCACAGACAATGTTAAACCATAATAGTACAGCTAAAT	7214	
Qy	892	GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACATAACAAGAAGGTTTATCTATA	951	
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Qy	1012	TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAG	1071	
Db	7335	TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAAG	7394	
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Db	7395	GAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAATT	7454	
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Qy	1192	AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA	1251	
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LOCUS	BD161892	Nonhuman primate	10501 bp	DNA linear PAT 17-JAN-2003
DEFINITION	BD161892	Nonhuman primate model of acquired immunodeficiency syndrome.		
ACCESSION	BD161892			
VERSION	BD161892.1	GI:27867650		
KEYWORDS	JP 2002159296-A/1.			
SOURCE	Simian-Human immunodeficiency virus			
ORGANISM	Simian-Human immunodeficiency virus			
REFERENCE	1 (bases 1 to 10501)			
AUTHORS	Shinohara,K., Sakai,K. and Honda,M.			
TITLE	Nonhuman primate model of acquired immunodeficiency syndrome			
JOURNAL	Patent: JP 2002159296-A 1 04-JUN-2002;			
COMMENT	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH			
	OS Simian-human immunodeficiency virus			
	PN JP 2002159296-A/1			
	PD 04-JUN-2002			
	PF 27-NOV-2000 JP 2000360274			
	PI KATSUAKI SHINOHARA,KOJI SAKAI,MITSUO HONDA			
	PC C12N15/09,A01K67/027,C12N7/00,C12N7/02,G01N33/15,G01N33/50//			
	PC G01N33/569,			
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	CC strain='SHIV-C2/1'			
	CC derived from Sivmac239			
	CC 5' long terminal repeat			
	CC U3 region			
	CC R region			
	CC U5 region			
	CC gag			
	CC pol			
	CC vif			
	CC vpx			
	CC vpr			
	CC derived from HIV-1			
	CC tat			
	CC rev			
	CC vpu			
	CC env			

CC	derived from SIVmac239	
CC	nef	
CC	3' long terminal repeat	
CC	U3 region	
CC	R region	
CC	U5 region	
FH	Key	Location/Qualifiers
FT	source	(1) . (10501)
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Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;		
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Db	7312	GAAGGAGAAATAAAAAATTGCTCTTCTATATCACCACAGCATAAAGAAATAAGGTAAG 7371
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Db	7372	AAAGAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAGTAAAAAATACTAGTAATACT 7431
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Db	7432	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC 7491
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RESULT 7  
HIV1U39362  
LOCUS  
DEFINITION  
HIV1U39362 9713 bp DNA linear VRL 10-AUG-2000  
Human immunodeficiency virus type 1 proviral DNA, gag, pol, vif,  
vpr, vpu, env, tat, rev and nef genes, complete cds.

ACCESSION U39362 M96155  
VERSION U39362.2 GI:9409797  
KEYWORDS  
SOURCE  
ORGANISM Human immunodeficiency virus 1 (HIV-1)  
Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 5029)  
AUTHORS Collman,R.G. and Yoon,H.L.  
JOURNAL Unpublished  
REFERENCE 2 (bases 5030 to 9713)  
AUTHORS Kim,F.M., Kolson,D.L., Balliet,J.W., Srinivasan,A. and Collman,R.G.  
TITLE V3-independent determinants of macrophage tropism in a primary  
human immunodeficiency virus type 1 isolate  
JOURNAL J. Virol. 69 (3), 1755-1761 (1995)  
MEDLINE 95156606  
PUBMED 7853514  
REFERENCE 3 (bases 1 to 9713)  
AUTHORS Collman,R., Balliet,J.W., Gregory,S.A., Friedman,H., Kolson,D.L.,  
Nathanson,N. and Srinivasan,A.  
TITLE An infectious molecular clone of an unusual macrophage-tropic and  
highly cytopathic strain of human immunodeficiency virus type 1  
JOURNAL J. Virol. 66 (12), 7517-7521 (1992)  
MEDLINE 93059708  
PUBMED 1433527  
REMARK Describes the isolation of the full-length clone and virus strain  
89.6  
REFERENCE 4 (bases 1 to 9713)  
AUTHORS Collman,R.G.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-1995) Ronald G. Collman, Pulmonary & Critical  
Care Division, University of Pennsylvania, 522 Johnson Pavilion,  
3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA  
REFERENCE 5 (bases 1 to 9713)  
AUTHORS Collman,R.G.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-2000) Ronald G. Collman, Pulmonary & Critical  
Care Division, University of Pennsylvania, 522 Johnson Pavilion,  
3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA  
REMARK Sequence updated by submitter  
COMMENT On Jul 24, 2000 this sequence version replaced gi:1055029.  
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	Matches 1466; Conservative 0; Mismatches 9; Indels 3; Gaps 1;				
QY	72	CATGCTCCTTGGGATATTGATGATCTGTAGTGCT---	ACAGAAAAAATTGTGGGTCACAGT	128	
Db	6273	CTTGCTCCTTGGGATGTTGATGATCTGTAGTGCTG	CAAAAGAAAAAACGTGGGTCACAAAT	6332	
QY	129	CTATTATGGGGTACCTGTGTGGAGAGAAGCAACCA	CCACTCTATTTTGTGCATCAGATGC	188	
Db	6333	CTATTATGGGTACCTGTGTGGAGAGAAGCAACCA	CCACTCTATTTTGTGCATCAGATGC	6392	
QY	189	TAAAGCCTATGATACAGAGGTACATAATGTTTT	GGGCCACACATGCCTGTGTACCCACAGA	248	
Db	6393	TAAAGCCTATGATACAGAGGTACATAATGTTTT	GGGCCACACATGCCTGTGTACCCACAGA	6452	
QY	249	CCCCAACCCACAAGAAGTAGTATTGGGAAATGTG	ACAGAAAAATTTTAACATGTGGAAAAA	308	
Db	6453	CCCCAACCCACAAGAAGTAGTATTGGGAAATGTG	ACAGAAAAATTTTAACATGTGGAAAAA	6512	
QY	309	TAACATGGTAGATCAGATGCATGAGGATATAATC	AGTTTATGGGATGAAAGCCTAAAGCC	368	

Db	6513	TAACATGGTAGATCAGATGCATGAGGATATAATC	AGTTTATGGGATGAAAGCCTAAAGCC	6572	
QY	369	ATGTGTAAAAATTAAACCCCACTCTGTGTTACT	TTTAAATTGCACCTAATTTGAATATCACTAA	428	
Db	6573	ATGTGTAAAAATTAAACCCCACTCTGTGTTACT	TTTAAATTGCACCTAATTTGAATATCACTAA	6632	
QY	429	GAATACTACTAATCCCACTAGTAGCAGCTGGG	GAATGATGGAGAAAAGGAGAAATAAAAAA	488	
Db	6633	GAATACTACTAATCCCACTAGTAGCAGCTGGG	GAATGATGGAGAAAAGGAGAAATAAAAAA	6692	
QY	489	TTGCTCTTTCTATATCACCAAGCATAAAGAA	ATAAGGTAAAAAGAAATATGCACTTT	548	
Db	6693	TTGCTCTTTCTATATCACCAAGCATAAAGAA	ATAAGGTAAAAAGAAATATGCACTTT	6752	
QY	549	TAATAGACTTGATGTAGTACCAATAGAAAA	TACTTAATAATCTAAGTATAGGTTAATAAG	608	
Db	6753	TAATAGACTTGATGTAGTACCAATAGAAAA	TACTTAATAATCTAAGTATAGGTTAATAAG	6812	
QY	609	TTGTAACACCTCAGTCATTACACAGGCCTGT	CCTCCAAAGGTATCCTTTCAGCCAATTC	668	
Db	6813	TTGTAACACCTCAGTCATTACACAGGCCTGT	CCTCCAAAGGTATCCTTTTCAGCCAATTC	6872	
QY	669	ACATTATTGTGTCCCGCTGGGTTTGC	GATGCTTAAAGTGTAAACAATAAGACATTC	728	
Db	6873	ACATTATTGTGTCCCGCTGGGTTTGC	GATGCTTAAAGTGTAAACAATAAGACATTC	6932	
QY	729	ATCAGGACCATGCACAAATGT	CAGCACAGTACAATGTACACATGGAATTAGGCCAGTGGT	788	
Db	6933	ATCAGGACCATGCACAAATGT	CAGCACAGTACAATGTACACATGGAATTAGGCCAGTGGT	6992	
QY	789	GTCAACTCAACTGCTGTTAAATGGCAGT	CTAGCAGAGAAGACATAGTAATTAGATCTGA	848	
Db	6993	GTCAACTCAACTGCTGTTAAATGGCAGT	CTAGCAGAGAAGACATAGTAATTAGATCTGA	7052	
QY	849	AAATTTACAGACAAATGCTAAAA	CCATAATAGTACAGCTAAATGAATCTGTAGTAATTA	908	
Db	7053	AAATTTACAGACAAATGCTAAAA	CCATAATAGTACAGCTAAATGAATCTGTAGTAATTA	7112	
QY	909	TTGTACAAGACCCCAACAATAACAAGA	AGGTTATCTATAGGACCAGGGAGAGCAATT	968	
Db	7113	TTGTACAAGACCCCAACAATAACAAGA	AGGTTATCTATAGGACCAGGGAGAGCAATT	7172	
QY	969	TTATGCAAGAAGAAACATAATAGGAGAT	ATAAGACAAGCACATTGTAACATTAGTAGAGC	1028	
Db	7173	TTATGCAAGAAGAAACATAATAGGAGAT	ATAAGACAAGCACATTGTAACATTAGTAGAGC	7232	
QY	1029	AAAAATGGAATAACACTTTTACAACAGAT	AGTTTATAAAATTAAGAGAAAAATTTAGGAATA	1088	
Db	7233	AAAAATGGAATAACACTTTTACAACAGAT	AGTTTATAAAATTAAGAGAAAAATTTAGGAATA	7292	
QY	1089	AACAATAGCCTTTAATCAATCCTCAGGAG	GGGACCCAGAAAAATTGTAATGCACAGTTTAA	1148	
Db	7293	AACAATAGCCTTTAATCAATCCTCAGGAG	GGGACCCAGAAAAATTGTAATGCACAGTTTAA	7352	
QY	1149	TTGTGGAGGGGAATTCTTCTACTGTA	ATACAGCACAACTGTTTAATAGTACTTGGAAATGT	1208	
Db	7353	TTGTGGAGGGGAATTCTTCTACTGTA	ATACAGCACAACTGTTTAATAGTACTTGGAAATGT	7412	
QY	1209	TACTGGAGGGACAAATGGCACTGA	AGGAAATGACATAATCACACTCCAATGCAGAAATAA	1268	
Db	7413	TACTGGAGGGACAAATGGCACTGA	AGGAAATGACATAATCACACTCCAATGCAGAAATAA	7472	
QY	1269	ACAAATTATAAATATGTGGCAGAAAG	TAGGAAAAGCAATGTATGCCCTCCCATCACAGG	1328	
Db	7473	ACAAATTATAAATATGTGGCAGAAAG	TAGGAAAAGCAATGTATGCCCTCCCATCACAGG	7532	
QY	1329	ACAAATTAGATGTTTCATCAAATATT	TACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG	1388	
Db	7533	ACAAATTAGATGTTTCATCAAATATT	TACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG	7592	
QY	1389	TACTGAGACTGAGACTGAGATCTT	CAGACCTTGGAGGAGGAGATATGAGGGACAAATTTGGAG	1448	
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Db 7593 TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGACAATTGGAG 7652

QY 1449 AAGTGAATTATATAAATAGTAAGAAATTGAACCAATAGGAGTAGCACCACCAG 1508

Db 7653 AAGTGAATTATATAAATAGTAAGAAATTGAACCAATAGGAGTAGCACCACCAG 7712

QY 1509 GGCAAAGAGAAGAACAGTGCAAAGAGAAAAAGACCGG 1546

Db 7713 GGCAAAGAGAAGAACAGTGCAAAGAGAAAAAGAGCAG 7750

RESULT 8

CQ753923

LOCUS CQ753923 2010 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 28 from Patent WO2004001051.

ACCESSION CQ753923

VERSION CQ753923.1 GI:44845222

KEYWORDS

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1

AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.

TITLE Recombinant measles viruses expressing epitopes of antigens of rna viruses - use for the preparation of vaccine compositions

JOURNAL Patent: WO 2004001051-A 28 31-DEC-2003;

INSTITUT PASTEUR (FR)

FEATURES

source Location/Qualifiers

1. .2010

/organism="Human immunodeficiency virus 1"

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ORIGIN

Query Match 66.0%; Score 1339.4; DB 6; Length 2010;

Best Local Similarity 94.5%; Pred. No. 1.5e-268;

Matches 1413; Conservative 0; Mismatches 46; Indels 36; Gaps 1;

QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111

Db 37 TGGGGGTGGAGATGGGGCCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 96

QY 112 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171

Db 97 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 156

QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACAT 231

Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216

QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATGGGAAATGTGACAGAAAAT 291

Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATGGGAAATGTGACAGAAAAT 276

QY 292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351

Db 277 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336

QY 352 GATGAAAGCCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCAC 411

Db 337 GATGAAAGCCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTAAATTGCAC 396

QY 412 AATTGAAATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG 471

Db 397 AATTGAAATATCACTAAGAAATACTACTAATCTCACTAGTAGCAGCTGGGGAATGATGGAG 456

QY 472 AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAAGAAATAAGGTAAAG 531

Db 457 GAAGGAGAAATAAAAAATTGCTCTTCTATATCACCAAGCATAAGAAATAAGGTAAAG 516

QY 532 AAAGAATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAATACT 591

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Db 697 AATAAGACATTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACAT 756

QY 772 GGAATTAGGCCAGTGGTGTCAAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAC 831

Db 757 GGAATTAGGCCAGTGGTGTCAAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAAC 816

QY 832 ATAGTAATTAGATCTGAAAAATTTTCACAGACAAATGCTAAAAACCATAATAGTACAGCTAAAT 891

Db 817 ATAGTAATTAGATCTGAAAGATTTTCACAGACAATGTTAAAAACCATAATAGTACAGCTAAAT 876

QY 892 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAATAACAAGAAAGGTTATCTATA 951

Db 877 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAATAACAATGC----- 917

QY 952 GGACCAGGAGAGCATTTTATGCAAGAAGAAACAATAATAGGAGATATAAGACAAGCACAT 1011

Db 918 -----TGCAGAAATTGGATAAAATGGGCAAGTGTGCAAGACAAAGCACAT 960

QY 1012 TGTAACATTAGTAGAGCAAAAATGGAATAAACACTTTTACAACAGATAGTTATAAAATTAAAGA 1071

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QY 1072 GAAAAATTTAGGAATAAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATT 1131

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Db 1141 AATAGTACTTGGAAATGTTCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1200

QY 1252 CTCCAATGCAGAAATAAACAAATATATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1311

Db 1201 CTCCAATGCAGAAATAAACAAATATATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1260

QY 1312 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATAATTTACAGGGCTGCTACTAACA 1371

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Db 1381 ATGAGGGACAATTGGAGAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1440

QY 1492 GGAGTAGCACCCACCAGGCAAAAGAGAAGAACAGTGCAAAAGAGAAAAAGACCGG 1546

Db 1441 GGAGTAGCACCCACCAGGCAAAAGAGAAGAACAGTGCAAAAGAGAAAAAGAGCAG 1495

RESULT 9

CQ753925

LOCUS CQ753925 2574 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 30 from Patent WO2004001051.

ACCESSION CQ753925

VERSION CQ753925.1 GI:44845223

KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1  
AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.  
TITLE Recombinant measles viruses expressing epitopes of antigens of rna  
viruses - use for the preparation of vaccine compositions  
JOURNAL Patent: WO 2004001051-A 30 31-DEC-2003;  
INSTITUT PASTEUR (FR)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 66.0%; Score 1339.4; DB 6; Length 2574;  
Best Local Similarity 94.5%; Pred. No. 1.4e-268;  
Matches 1413; Conservative 0; Mismatches 46; Indels 36; Gaps 1;  
QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111  
Db 37 TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 96  
QY 112 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTA 171  
Db 97 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTA 156  
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACAT 231  
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QY 472 AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAAGAAAAATAGGTAAAG 531  
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QY 952 GGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAAGGAGATATAAGACAAGCACAT 1011  
Db 918 -----TGCAGAATTGGATAAAATGGGCAAGTGTGCAAGACAAGCACAT 960  
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Db 961 TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGA 1020  
QY 1072 GAAAAATTTAGGAATAAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCCAAAAATT 1131  
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RESULT 10  
AY247221  
LOCUS HIV-1 isolate 81NJ from USA envelope glycoprotein (env) gene, 2553 bp DNA linear VRL 16-MAY-2003  
DEFINITION complete cds.  
ACCESSION AY247221  
VERSION AY247221.1 GI:30794652  
KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 2553)  
AUTHORS Robbins,K.E., Lemey,P., Pybus,O.G., Jaffe,H.W., Youngpairaj,A.S., Brown,T.M., Salemi,M., Vandamme,A.M. and Kalish,M.L.  
TITLE U.s. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains  
JOURNAL J. Virol. 77 (11), 6359-6366 (2003)  
MEDLINE 22628496  
PUBMED 12743293  
REFERENCE 2 (bases 1 to 2553)  
AUTHORS Robbins,K.E.  
TITLE Direct Submission



JOURNAL Submitted (04-MAR-2003) NCID/DASTLR/HARB/VETS, Centers for Disease Control & Prevention, 1600 Clifton Rd., Mail Stop G-19, Atlanta, GA 30333, USA

FEATURES  
source

Location/Qualifiers

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ORIGIN

Query Match 62.3%; Score 1262.8; DB 14; Length 2553;  
Best Local Similarity 92.1%; Pred. No. 1.3e-252;  
Matches 1369; Conservative 0; Mismatches 102; Indels 15; Gaps 3;

QY	64	TCGAGATCCATGCTCCITGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGCGGTC	123
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QY	124	ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACTCTATTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCACTCTATTTTGTGCATCA	165
QY	184	GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC	243
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QY	244	ACAGACCCCAACCCACAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGG	303
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QY	304	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
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QY	364	AAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATAATTTGAATATC	423
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RESULT 11  
AY426111

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QY	661	ATTCCCATACATTATTGTGTCCCGGCTGGGTTTGGCATGCTAAAAGTGTAAACAATAAGACA	720
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QY	781	CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATT	840
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QY	841	AGATCTGAAAAATTTTCAGACACAATGCTAAAAACCATAATAGTACAGTAAAATGAATCTGTA	900
Db	817	AGATCTGACAATTTTCACGACAAATGCTAAAAACCATAATAGTACAGCTGAAAGAATCTGTA	876
QY	901	GTAATTAATTGTACAAAGACCCAAACAATACAAGAAAGGTTATCTATAGGACCAAGG	960
Db	877	GAAATTAATTGTACAAAGACCCAAACAATACAAGAAAAAGTATACATATAGGACCAAGG	936
QY	961	AGAGCATTTTATGCAAGAAAGAAAAATAATAGGAGATATAAGACAAGCACATTGTAAACATT	1020
Db	937	AGAGCATTTTATACAAAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAAACCTT	996
QY	1021	AGTAGAGCAAAATGGAATAACACCTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTT	1080
Db	997	AGTAGAGCAAAATGGGATAACACCTTTAAAACAGATAGTTAGAAAAATTAAGAGAACAAATTT	1056
QY	1081	AGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAATGCAC	1140
Db	1057	GGGAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAAACGCAC	1116
QY	1141	AGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAAATACAGCACAACTGTTTAATAGTACT	1200
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QY	1201	TGGAATGTTACTGGAGGGACAAAATGGCACCTGAAGGAAATGACATAATCACACTCCAATGC	1260
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QY	1261	AGAAATAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAAAAAGCAATGTATGCCCTCCC	1320
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QY	1441	AATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA	1500
Db	1414	AATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCATTTAGGAGTAGCA	1473
QY	1501	CCCACCAGGGCAAAAGAGAAGAACAGTGCAAAAGAGAGAAAAAGACCGG	1546
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LOCUS	AY426111	2568 bp	DNA	linear	VRL 28-JUN-2004
DEFINITION	HIV-1 clone BaL-lp isolate BaL from USA envelope glycoprotein (env) gene, complete cds.				
ACCESSION	AY426111				
VERSION	AY426111.1	GI:37962967			
KEYWORDS					
SOURCE	Human immunodeficiency virus 1 (HIV-1)				
ORGANISM	Human immunodeficiency virus 1				
REFERENCE	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.				
AUTHORS	1 (bases 1 to 2568)				
TITLE	Pastore,C., Ramos,A. and Mosier,D.E.				
JOURNAL	Intrinsic Obstacles to Human Immunodeficiency Virus Type 1				
PUBMED	Coreceptor Switching				
REFERENCE	J. Virol. 78 (14), 7565-7574 (2004)				
AUTHORS	15220431				
TITLE	2 (bases 1 to 2568)				
JOURNAL	Pastore,C., Ramos,A. and Mosier,D.E.				
FEATURES	Direct Submission				
source	Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA				
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ORIGIN									
Query Match	61.3%;	Score	1242.2;	DB	14;	Length	2568;		
Best Local Similarity	90.2%;	Pred.	No. 2.4e-248;						
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Qy	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA	171						
Db	97	AAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGCAACCACTCTA	156						
Qy	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231						
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Query Match	61.3%	Score	1242.2;	DB 14;	Length	2568;
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Dd	37	TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTTGATGATCTGTAGTGCTACAGAA	96			
Qy	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA	171			
Dd	97	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTA	156			
Qy	172	TTTTTGTGCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231			
Dd	157	TTTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT	216			

Qy	232	GCCTGTGTACCCACAGACCCCCAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAAT	291			
Dd	217	GCCTGTGTACCCACAGACCCCCAACCCACAAGAAAGTAGAATTGGAAAAATGTGACAGAAAAAT	276			
Qy	292	TTTAACATGTGGAAAAATAAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351			
Dd	277	TTTAACATGTGGAAAAATAAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGG	336			
Qy	352	GATGAAAGCCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTCGCACT	411			
Dd	337	GATCAAAGCCCTAAAGCCATGTGTAAAAATTAACTCCACTCTGTGTTACTTTAAATTCGCACT	396			
Qy	412	AATTTGAATATCACTA-----AGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG	465			
Dd	397	GATTTGAGGAATACTACTAATGGGAATGACACTAATACCACTAGTAGTAGCAGGGAATG	456			
Qy	466	ATGGAGAAAGGAGAAATAAAAAAATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAG	525			
Dd	457	ATGGGGGAGGAGAAATGAAAAAATTGCTCTTTCAAATAACCCACAACATAAGAGGTAAAG	516			
Qy	526	GTAAGAAAGAAATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATACTAAT	585			
Dd	517	GTGCAGAAAGAAATATGCACCTTTTATAAACTTGTATATAGTACCAATAGATAATAATAGT	576			
Qy	586	AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAG	645			
Dd	577	AATAATAGATATAGGTTGATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAG	636			
Qy	646	GTATCCTTTCAGCCCAATCCCATACATTATTGTGTCCCGCTGGGTTTTCGATGCTTAAAG	705			
Dd	637	ATATCCTTTGAGCCCAATCCCATACATTATTGTGCCCCGGCTGGTTTTTTCGATTTCTAAAG	696			
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Dd	697	TGTAAGAATAAGAAAGTTCAATGGAAAAGGACCATGTTCAAATGTCAGCACAGTACAATGT	756			
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Dd	817	GAAGAGGTAGTAATTAGATCCGAAAAATTTTCGCGGACAAATGCTAAAAACCATAATAGTACAG	876			
Qy	886	CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTA	945			
Dd	877	CTGAATGAATCTGTAGAAATTAATTGTACAAGACCCCAACAACAATAACAAGAAAGTATA	936			
Qy	946	TCTATAGGACCAGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA	1005			
Dd	937	CATATAGGACCAGGACAGCATTATATACAAACAGGAAAAATAATAGGAGATATAAGACAA	996			
Qy	1006	GCACATTGTAACATTAGTAGAGCAAAAATGGAATAACACTTTACAAACAGATAGTTATAAAA	1065			
Dd	997	GCACATTGTAACCTTAGTAGAGCAAAAATGGAATGACACTTTAAATAAGATAGTTATAAAA	1056			
Qy	1066	TTAAGAGAAAAAATTTAGGAATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGACCCA	1125			
Dd	1057	TTAAGAGAACAAATTTGGGAATAAAAACAATAGTCTTTTAAGCATTCCTCAGGAGGGACCCA	1116			
Qy	1126	GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAA	1185			
Dd	1117	GAAATTGTGACGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATTCACACAA	1176			
Qy	1186	CTGTTTAATAGTACTTGGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAATGACATA	1245			
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Qy	1246	ATCACACTCCAATGCAGATAAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCA	1305			
Dd	1237	ATCACACTCCCATGCAGATAAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAAAAGCA	1296			
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QY 1426 GGAGATATGAGGGACAATTGGAGAAAGTGAATTATATAAAATATAAAAGTAGTAAGAAATTGAA 1485  
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QY 1486 CCAATAGGAGTAGCACCCACCGGCAAGAGAGAAAGACAGTGCAAAGAGAGAAAAAGACCG 1545  
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RESULT 12  
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LOCUS  
DEFINITION HIV-1 clone BaL-1A isolate BaL from USA envelope glycoprotein (env)  
gene, complete cds.  
ACCESSION AY426112  
VERSION AY426112.1 GI:37962969  
KEYWORDS  
SOURCE  
ORGANISM Human immunodeficiency virus 1 (HIV-1)  
Human immunodeficiency virus 1  
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
lentivirus group.  
REFERENCE 1 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1  
Coreceptor Switching  
J. Virol. 78 (14), 7565-7574 (2004)  
JOURNAL  
PUBMED 15220431  
REFERENCE 2 (bases 1 to 2568)  
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.  
TITLE Direct Submission  
Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research  
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA  
JOURNAL  
Location/Qualifiers  
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ORIGIN

Query Match 61.2%; Score 1240.6; DB 14; Length 2568;  
Best Local Similarity 90.1%; Pred. No. 5.2e-248;  
Matches 1353; Conservative 0; Mismatches 139; Indels 9; Gaps 2;

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QY 112 AAATTGTGGTCCAGTCTTATTATGGGTACCTGTGTGGAGAGAAAGCAACCCACTCTA 171  
Db 97 AAATTGTGGTCCAGTCTTATTATGGGTACCTGTGTGGAAAGAAAGCAACCCACTCTA 156  
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QY	1066	TTAAGAGAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCCA	1125
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QY	1426	GGAGATATGAGGGACAATTTGGAGAAGTGAATTTATATAAAATATAAAGTAGTAAGAATTGAA	1485
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QY	1486	CCAATAGGAGTAGCACCCACCAGGGCAAAGAGAGAACAGTGTCAAAGAGAAAAAGACCG	1545
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QY	1546	G	1546
Db	1534	G	1534

RESULT 13	
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LOCUS	AY426118.1
DEFINITION	HIV-1 clone BaL-4p isolate BaL from USA envelope glycoprotein (env) gene, complete cds.
ACCESSION	AY426118
VERSION	AY426118.1
KEYWORDS	GI:37962981
SOURCE	Human immunodeficiency virus 1 (HIV-1)
ORGANISM	Human immunodeficiency virus 1
REFERENCE	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
AUTHORS	1 (bases 1 to 2568)
TITLE	Pastore,C., Ramos,A. and Mosier,D.E.
JOURNAL	Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
PUBMED	Coreceptor Switching
REFERENCE	J. Virol. 78 (14), 7565-7574 (2004)
AUTHORS	15220431
TITLE	2 (bases 1 to 2568)
JOURNAL	Pastore,C., Ramos,A. and Mosier,D.E.
FEATURES	Direct Submission
source	Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
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		Query Match 61.1%; Score 1239; DB 14; Length 2568;	
		Best Local Similarity 90.1%; Pred. No. 1.1e-247;	
		Matches 1352; Conservative 0; Mismatches 140; Indels 9; Gaps 2;	
QY	52	TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA	111
Db	37	TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA	96
QY	112	AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCACACTCTA	171
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QY	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGCCACACAT	231
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Db	217	GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGAATTGGAAAATGTGACAGAAAAAT	276
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QY	412	AAATTGA-----ATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG	465
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QY	526	GTAAGAAAGAATATGCACCTTTTAAATAGACTTTTGTAGTACCAATAGAAAAATACTAAT	585
Db	517	GTGAGAAAGAATATGCACCTTTTATAAATTTGATATAGTACCAATAGATAATAATAGT	576
QY	586	AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAG	645
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Db 1534 G 1534

RESULT 14

AY426110

LOCUS AY426110 2568 bp DNA linear VRL 28-JUN-2004

DEFINITION HIV-1 isolate BaL from USA envelope glycoprotein (env) gene, complete cds.

ACCESSION AY426110

VERSION AY426110.1 GI:37962965

KEYWORDS Human immunodeficiency virus 1 (HIV-1)

SOURCE

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate

lentivirus group.

REFERENCE 1 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching

JOURNAL J. Virol. 78 (14), 7565-7574 (2004)

PUBMED 15220431

REFERENCE 2 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 61.0%; Score 1237.4; DB 14; Length 2568;

Best Local Similarity 90.0%; Pred. No. 2.4e-247;

Matches 1351; Conservative 0; Mismatches 141; Indels 9; Gaps 2;

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Db 37 TGGGGTGGAGATGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 96

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Db 757 ACACATGGGATTAGGCCAGTAGTATCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAA 816

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Db 877 CTGAATGAATCTGTAGAAATTAATTGTACAAGACCCCAACAATAACAAGAAAAAGTATA 936

Qy 946 TCTATAGGACCAGGAGAGCAATTTTATGCAAGAAGAAACATAAATAGGAGATATAAGCAA 1005

Db 937 CATATAGGACCAGGCAGACATTATATACAACAGGAGAAATAATAGGAGATATAAGCAA 996

Qy 1006 GCACATTGTAACATTAGTAGAGCAAAAAATGAATAACACTTTACAACAGATAGTTATAAAA 1065

Db 997 GCACATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTAAATAAGATAGTTATAAAA 1056

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Db 1357 TTAACAAGAGATGGTGG---TCCAGAGGACAACAAGACCGAGGTCTTCAGACCTGGAGGA 1413

Qy 1426 GGAGATATGAGGGACAAATTGGGAAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAA 1485

Db 1414 GGAGATATGAGGGACAAATTGGGAAGTGAATTATATAATAATAAAGTAGTAAAAAATTGAA 1473

Qy 1486 CCAATAGGAGTAGCACCCACGAGGCAAGAGAGAAAGACAGTGCAAGAGAAAAAGACCG 1545

Db 1474 CCATTAGGAGTAGCACCCACCAAGGCAAGAGAGAGAGTGGTGCAGAGAAAAAGAGCA 1533

Qy 1546 G 1546

Db 1534 G 1534

RESULT 15

LOCUS AY426113

DEFINITION HIV-1 clone BaL-1B isolate BaL from USA envelope glycoprotein (env) gene, complete cds.

ACCESSION AY426113

VERSION AY426113.1 GI:37962971

KEYWORDS .

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching

JOURNAL J. Virol. 78 (14), 7565-7574 (2004)

PUBMED 15220431

REFERENCE 2 (bases 1 to 2568)

AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

Location/Qualifiers

1..2568

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/proviral

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ORIGIN

Query Match 61.0%; Score 1237.4; DB 14; Length 2568;

Best Local Similarity 90.0%; Pred. No. 2.4e-247;

Matches 1351; Conservative 0; Mismatches 141; Indels 9; Gaps 2;



QY	52	TGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
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QY	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACTCTA	171
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QY	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
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QY	292	TTTAAACATGTGGAATAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
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GenCore version 5.1.6  
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SUMMARIES

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4	1786.4	88.1	2252	4	AAF82928
5	1453.4	71.7	2046	12	ACA63265
6	1453.4	71.7	2610	12	ACA63266
7	1447.6	71.4	2051	10	AAL56171
8	1447.6	71.4	2562	10	AAL56170
9	1339.4	66.0	2010	12	ACA63267
10	1339.4	66.0	2574	12	ACA63268
11	1225.4	60.4	3806	2	AAx04767
12	1225.4	60.4	3807	2	AAT58551
13	1221.8	60.2	9540	12	ADO52562
14	1221.8	60.2	9540	12	ADP20074
15	1219	60.1	3807	2	AAQ14753
16	1207.4	59.5	2553	1	AAH80949
17	1198.8	59.1	2612	12	ADJ92821
18	1198.8	59.1	8896	12	ADP20082
19	1197	59.0	1512	5	AAF87100
20	1179.8	58.2	1422	12	ADP74731
21	1174.2	57.9	3808	2	AAV58244

C	22	1174.2	57.9	3808	2	AAV60252	Aav60252 Insert re
	23	1172.6	57.8	2553	2	AAQ76018	Aaq76018 DNA encod
	24	1172.2	57.8	2571	2	AAT09010	Aat09010 HIV-1 str
	25	1172.2	57.8	2571	2	AZ08741	Aaz08741 HIV-1 MN
	26	1172.2	57.8	2571	3	AA93973	Aaa93973 Human imm
	27	1172.2	57.8	2571	4	AAC86877	Aac86877 Nucleotid
	28	1172.2	57.8	2571	5	AAH43700	Aah43700 Wild type
	29	1172.2	57.8	2571	8	ABX14499	Abx14499 Human imm
	30	1172.2	57.8	2571	9	ADA50072	Ada50072 Human imm
	31	1172.2	57.8	2571	10	ADE81077	Ade81077 HIV-1 (MN
	32	1172.2	57.8	2571	12	ADG92081	Adg92081 HIV rev/e
C	33	1172.2	57.8	6474	2	AAQ40300	Aaq40300 Sequence
C	34	1172.2	57.8	6474	3	AA89877	Aaa89877 Plasmid p
C	35	1172.2	57.8	6474	4	AA812795	Aaa12795 Plasmid p
	36	1172.2	57.8	6926	2	AAQ40281	Aaq40281 Sequence
	37	1172.2	57.8	6926	3	AA89880	Aaa89880 pP2-gp 16
	38	1172.2	57.8	6926	4	AA812798	Aaa12798 Plasmid p
	39	1172.2	57.8	9738	2	AAx04765	Aax04765 The compl
	40	1172.2	57.8	9739	2	AAT58549	Aat58549 Human Imm
	41	1172.2	57.8	9745	2	AAx04766	Aax04766 The compl
	42	1172.2	57.8	9746	2	AAQ14752	Aaq14752 HIV-1 (MN-
	43	1172.2	57.8	9746	2	AAT58550	Aat58550 Human Imm
	44	1169.4	57.7	2574	2	AAQ76019	Aaq76019 DNA encod
	45	1168.8	57.6	4527	2	AAT33899	Aat33899 HIV-1 SF3

ALIGNMENTS

RESULT 1  
AAF82931  
ID AAF82931 standard; CDNA; 2028 BP.  
XX  
AC AAF82931;  
XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX  
DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
CDS 13..2028  
FT /\*tag= a  
FT sig\_peptide 13..72  
FT /\*tag= b  
FT /note= "synthetic secretory signal peptide"  
FT misc\_feature 73..1542  
FT /\*tag= c  
FT /note= "HIV-1 gp120 domain coding sequence"  
FT misc\_feature 1543..1551  
FT /\*tag= d  
FT /note= "ProAspPro linker coding sequence"  
FT misc\_feature 1552..2028  
FT /\*tag= e  
FT /note= "human CD154 short form extracellular domain coding sequence"  
FT  
XX WO200126608-A2.  
PN  
XX  
PD 19-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028414.  
XX  
PR 14-OCT-1999; 99US-0159690P.  
XX  
PA (LEDB/) LEDBETTER J A.





Db 1741 ATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1800

Qy 1801 GCCAGCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAAT 1860

Db 1801 GCCAGCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAAT 1860

Qy 1861 ACCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 1920

Db 1861 ACCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 1920

Qy 1921 TTGCAACCAAGTGCTTCGGTGTGTTGTCAATGTGACTGATCCTCAAGCCAAAGTGAGCCATGGC 1980

Db 1921 TTGCAACCAAGTGCTTCGGTGTGTTGTCAATGTGACTGATCCTCAAGCCAAAGTGAGCCATGGC 1980

Qy 1981 ACTGGCTTCACGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2028

Db 1981 ACTGGCTTCACGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2028

RESULT 2

AAF82930

ID AAF82930 standard; cDNA; 2070 BP.

XX

AC AAF82930;

XX

DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX

DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.

XX

KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX

OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..2070

FT /\*tag= a

FT sig\_peptide 13..72

FT /\*tag= b

FT /\*note= "synthetic secretory signal peptide"

FT misc\_feature 73..1542

FT /\*tag= c

FT /\*note= "HIV-1 gp120 domain coding sequence"

FT misc\_feature 1543..1593

FT /\*tag= d

FT /\*note= "[Gly4Ser]3 linker coding sequence"

FT misc\_feature 1594..2070

FT /\*tag= e

FT /\*note= "human CD154 short form extracellular domain coding sequence"

XX

PN WO200126608-A2.

XX

PD 19-APR-2001.

XX

PF 13-OCT-2000; 2000WO-US028414.

XX

PR 14-OCT-1999; 99US-0159690P.

XX

PA (LEDB/) LEDBETTER J A.

PA (HAYD/) HAYDEN-LEDBETTER M S.

XX

PI Ledbetter JA, Hayden-Ledbetter MS;

DR WPI; 2001-281790/29.

DR P-PSDB; AAB62335.

XX

PT DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PT

XX Example 1; Fig 3B; 55pp; English.

PS The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by (Gly4Ser)3 linker. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;

Query Match 97.3%; Score 1972.8; DB 4; Length 2070;

Best Local Similarity 97.9%; Pred. No. 0;

Matches 2026; Conservative 0; Mismatches 2; Indels 42; Gaps 1;

Qy 1 AAGCTTGGCCCATGCTGTATACCTCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Db 1 AAGCTTGGCCCATGCTGTATACCTCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Qy 61 GCTTCGAGATCCATGCTCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCTATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGG 120

Qy 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACACCACCCTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACACCACCCTCTATTTTGTGCA 180

Qy 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCTGTGTA 240

Db 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCTGTGTA 240

Qy 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAATGTGACAGAAAAATTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAATGTGACAGAAAAATTTAACATG 300

Qy 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTATGGGATGAAAGC 360

Qy 361 CTAAAGCCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTTGAAT 420

Db 361 CTAAAGCCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTTGAAT 420

Qy 421 ATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAA 480

Db 421 ATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAA 480

Qy 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAATAAAGGTAAGAAAGAATAT 540

Db 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAATAAAGGTAAGAAAGAATAT 540

Qy 541 GCACCTTTTAAATAGACTGTAGTACCAATAGAAAAATACTAATACTAAGTATAGG 600

Db 541 GCACCTTTTAAATAGACTGTAGTACCAATAGAAAAATACTAATACTAAGTATAGG 600

Qy 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTCAGCCA 660

Db 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTCAGCCA 660

Qy 661 ATTCCCATACATTATTGTGTCCCGCTGGGTTTGCATGCTAAAAGGTATCCTTTCAGCCA 720

Db 661 ATTCCCATACATTATTGTGTCCCGCTGGGTTTGCATGCTAAAAGGTATCCTTTCAGCCA 720

Qy 721 TTCAATGGATCAGGACCATGCAAAATGTGAGTACAGTACCAATGTGCAATGGAATTAGG 780

Db 721 TTCAATGGATCAGGACCATGCAAAATGTGAGTACAGTACCAATGTGCAATGGAATTAGG 780

Qy 781 CCAGTGGTGTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840

Db 781 CCAGTGGTGTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840

QY	841	AGATCTGAAAATTTACAGACAATGCTAAAAACCATATAATAGTACAGCTAAATGAATCTGTA	900
Db	841		
QY	901	GTAATTAATTGTACAAGACCCAAACAACAATACAAGAAGAAGGTTATCTATAGGACCAGGG	960
Db	901		
QY	961	AGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAAACATT	1020
Db	961		
QY	1021	AGTAGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTT	1080
Db	1021		
QY	1081	AGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAATGCAC	1140
Db	1081		
QY	1141	AGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAATACAGACAACACTGTTTAAATAGTACT	1200
Db	1141		
QY	1201	TGGAATGTTACTGGAGGGACAATGGCACTGAAGGAATGACATAATCACACTCCAATGC	1260
Db	1201		
QY	1261	AGATAAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCC	1320
Db	1261		
QY	1321	ATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGTGCTACTAAACAAGAGATGGA	1380
Db	1321		
QY	1381	GGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGGAGAGATATGAGGGAC	1440
Db	1381		
QY	1441	AAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA	1500
Db	1441		
QY	1501	CCCAACAGGGCAAAAGAGAAACAAGTGCAAAAGAGAAAAA-----	1540
Db	1501		
QY	1541	-----GACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGT	1578
Db	1561	GGTGGAGGTTCTGGAGGTGGCGGATCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGT	1620
QY	1579	GATCAGAATCCTCAAATTGCGGCACATGTCATAAGTGAAGCCAGCAGTAAAAACAACATCT	1638
Db	1621		
QY	1639	GTGTTACAGTGGCTGAAAAAGGATACACCATGAGCAACAACCTTGGTAACCCCTGGAA	1698
Db	1681	GTGTTACAGTGGGCTGAAAAAGGATACACCATGAGCAACAACCTTGGTAACCCCTGGAA	1740
QY	1699	AATGGGAAACAGCTGACCCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACC	1758
Db	1741	AATGGGAAACAGCTGACCCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACC	1800
QY	1759	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAG	1818
Db	1801	TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAG	1860
QY	1819	TCCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAA	1878
Db	1861	TCCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAA	1920
QY	1879	CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCG	1938
Db	1921		
QY	1939	GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTT	1998
Db	1981	GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTT	2040
QY	1999	GGCTTACTCAAACCTCGAGTGATAATCTAGA	2028
Db	2041	GGCTTACTCAAACCTCGAGTGATAATCTAGA	2070
RESULT 3			
AAF82929			
ID	AAF82929	standard; cDNA; 2209 BP.	
XX			
AC	AAF82929;		
XX			
DT	11-SEP-2003	(revised)	
DT	29-JUN-2001	(first entry)	
XX			
DE	HIV-1	gpl20-human CD154 long form extracellular domain fusion cDNA.	
XX			
KW	Antigen; receptor; humoral; cellular; immune response; DNA vaccine;		
KW	acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;		
KW	HIV-1; gp120; human; CD154; fusion protein; ss.		
XX			
OS	Human immunodeficiency virus 1.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CDS	13..2209		
FT			
FT	/tag= a		
FT	13..72		
FT	/tag= b		
FT	/note= "synthetic secretory signal peptide"		
FT	73..1542		
FT	/tag= c		
FT	/note= "HIV-1 gp120 domain coding sequence"		
FT	1543..1551		
FT	/tag= d		
FT	/note= "ProAspPro linker coding sequence"		
FT	1552..2209		
FT	/tag= e		
FT	/note= "human CD154 long form extracellular domain coding sequence"		
FT			
XX			
PN	WO200126508-A2.		
XX			
PD	19-APR-2001.		
XX			
PF	13-OCT-2000; 2000WO-US028414.		
XX			
PR	14-OCT-1999; 99US-0159690P.		
XX			
PA	(LEDB/) LEDBETTER J A.		
PA	(HAYD/) HAYDEN-LEDBETTER M S.		
XX			
PI	Ledbetter JA, Hayden-Ledbetter MS;		
XX			
DR	WPI; 2001-281790/29.		
DR	P-PSDB; AAB62334.		
XX			
PT	DNA vaccine for improving antigen-specific humoral and cellular immune		
PT	responses, comprising one or more antigens linked to a domain that binds		
PT	at least one receptor.		
XX			
PS	Example 1; Fig 3A; 55pp; English.		
XX			
CC	The invention provides a vaccine comprising one or more antigens linked		
CC	to a domain that binds at least one receptor to improve the antigen-		
CC	specific humoral and cellular immune response. The DNA vaccines induce		



CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC long form extracellular domain fusion protein linked by a ProAspPro  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
XX

SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;

Query Match 90.6%; Score 1838; DB 4; Length 2209;  
Best Local Similarity 91.8%; Pred. No. 0;  
Matches 2028; Conservative 0; Mismatches 0; Indels 180; Gaps 1;

Qy	1	AAGTTGCGGCCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTTGGATCTCG	60
Db	1	AAGTTGCGGCCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTTGGATCTCG	60
Qy	61	GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTGTGG	120
Db	61	GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTGTGG	120
Qy	121	GTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA	180
Db	121	GTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA	180
Qy	181	TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGCCACACATGCCTGTGTA	240
Db	181	TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGCCACACATGCCTGTGTA	240
Qy	241	CCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATG	300
Db	241	CCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATG	300
Qy	301	TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC	360
Db	301	TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC	360
Qy	361	CTAAAGCCATGTGTAATAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATAATTGAAT	420
Db	361	CTAAAGCCATGTGTAATAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATAATTGAAT	420
Qy	421	ATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA	480
Db	421	ATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA	480
Qy	481	ATAAAAAAATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGAAAGATAT	540
Db	481	ATAAAAAAATTGCTCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAAGAAAGATAT	540
Qy	541	GCACCTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGG	600
Db	541	GCACCTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGG	600
Qy	601	TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTACGCCA	660
Db	601	TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTACGCCA	660
Qy	661	ATTCCCATACATTATTGTGTCCTGGCTGGGTTTGGGATGCTTAAAGTGTAAACAATAAGACA	720
Db	661	ATTCCCATACATTATTGTGTCCTGGCTGGGTTTGGGATGCTTAAAGTGTAAACAATAAGACA	720
Qy	721	TTCAATGGATCAGGACCATGCAAAATGTGAGCACAGTACATAATGTACACATGGAATTAGG	780
Db	721	TTCAATGGATCAGGACCATGCAAAATGTGAGCACAGTACATAATGTACACATGGAATTAGG	780
Qy	781	CCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT	840
Db	781	CCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT	840
Qy	841	AGATCTGAAAAATTTCACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA	900
Db	841	AGATCTGAAAAATTTCACAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTA	900
Qy	901	GTAATTAATTGTACAAGACCCCAACAACATAACAAGAAAGGTTATCTATAGGACCGGG	960

Db	901	GTAATTAATTGTACAAGACCCCAACAACATAACAAGAAAGGTTATCTATAGGACCGGG	960
Qy	961	AGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAAACATT	1020
Db	961	AGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAAACATT	1020
Qy	1021	AGTAGAGCAAAATGGAATAACACCTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTT	1080
Db	1021	AGTAGAGCAAAATGGAATAACACCTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTT	1080
Qy	1081	AGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCAC	1140
Db	1081	AGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCAC	1140
Qy	1141	AGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATACAGCACAACTGTTTAATAGTACT	1200
Db	1141	AGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATACAGCACAACTGTTTAATAGTACT	1200
Qy	1201	TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC	1260
Db	1201	TGGAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC	1260
Qy	1261	AGAAATAAAACAATTAATAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCC	1320
Db	1261	AGAAATAAAACAATTAATAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCC	1320
Qy	1321	ATCACAGGACAAATTAGATGTTTCAATCAATATTACAGSGCTGTACTAAACAAGAGATGGA	1380
Db	1321	ATCACAGGACAAATTAGATGTTTCAATCAATATTACAGSGCTGTACTAAACAAGAGATGGA	1380
Qy	1381	GGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGAC	1440
Db	1381	GGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGAC	1440
Qy	1441	AATTGGAGAAAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA	1500
Db	1441	AATTGGAGAAAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCA	1500
Qy	1501	CCCACAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGACCGGATCC-----	1550
Db	1501	CCCACAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGACCGGATCCCAAGAAGGTTG	1560
Qy	1551	-----	1550
Db	1561	GACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCATGAAAAACGATACAG	1620
Qy	1551	-----	1550
Db	1621	AGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAGCCAG	1680
Qy	1551	-----	1560
Db	1681	TTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGAGACGAAGAAAGAAAAACAGC	1740
Qy	1561	TTTGAAGGCTTTGTGAAGGATCAGAAATCCTCAAAATTTGGCGCACATGTCTAAGTGAGGCC	1620
Db	1741	TTTGAAGGCTTTGTGAAGGATCAGAAATCCTCAAAATTTGGCGCACATGTCTAAGTGAGGCC	1800
Qy	1621	AGCAGTAAAAACAACATCTGTGTTACAGTGGCTGAAAAAGGATACTACACCATGAGCAAC	1680
Db	1801	AGCAGTAAAAACAACATCTGTGTTACAGTGGCTGAAAAAGGATACTACACCATGAGCAAC	1860
Qy	1681	AACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT	1740
Db	1861	AACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTAT	1920
Qy	1741	ATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAGAGCTTCGAGTCAAGCTCCATTATA	1800
Db	1921	ATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAGAGCTTCGAGTCAAGCTCCATTATA	1980
Qy	1801	GCCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAAT	1860

Db 1981 GCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACTCAGAGCTGCAAAAT 2040

QY 1861 ACCACAGTTCCGCCAAACCTTCGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 1920

Db 2041 ACCACAGTTCCGCCAAACCTTCGGGCAACAATCCATTCACTTGGGAGGAGTATTGAA 2100

QY 1921 TTGCAACCAAGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCAAGTGAGCCATGGC 1980

Db 2101 TTGCAACCAAGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCAAGTGAGCCATGGC 2160

QY 1981 ACTGGCTTCACGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2028

Db 2161 ACTGGCTTCACGTCCTTTGGCTTACTCAAACTCGAGTGATAATCTAGA 2208

RESULT 4

AAF82928

ID AAF82928 standard; cDNA; 2252 BP.

XX

AC AAF82928;

XX

DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX

DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.

XX

KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX

OS Human immunodeficiency virus 1.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..2252

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CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC long form extracellular domain fusion protein linked by (Gly4Ser)3  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;

Query Match 88.1%; Score 1786.4; DB 4; Length 2252;  
Best Local Similarity 89.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 6; Indels 222; Gaps 1;

QY 1 AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTTGGATCTCG 60

Db 1 AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTTGGATCTCG 60

QY 61 GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

Db 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGG 120

QY 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACCTCTATTTTGTGCA 180

Db 121 GTCACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACCTCTATTTTGTGCA 180

QY 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTA 240

Db 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTA 240

QY 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

Db 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATG 300

QY 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

Db 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGC 360

QY 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAAT 420

Db 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAAT 420

QY 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

Db 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAA 480

QY 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATTAAGTAAGTAAGTAAGTAAGTAAT 540

Db 481 ATAAAAAATTGCTCTTTCTATATCACCACAAGCATTAAGTAAGTAAGTAAGTAAGTAAT 540

QY 541 GCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAACTAAGTATAGG 600

Db 541 GCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAATAACTAAGTATAGG 600

QY 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660

Db 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCA 660

QY 661 ATTCCCATACATTATTGTGTCCCGGTGGTTTGGAGTGCTAAAGTGTAAACAATAAGACA 720

Db 661 ATTCCCATACATTATTGTGTCCCGGTGGTTTGGAGTGCTAAAGTGTAAACAATAAGACA 720

QY 721 TTCAATGGATCAGGACCATGCACAAATGTTCAGCACAGTACAAATGTACACATGGAATTAGG 780

Db 721 TTCAATGGATCAGGACCATGCACAAATGTTCAGCACAGTACAAATGTACACATGGAATTAGG 780

QY 781 CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATT 840

Db 781 CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATT 840

QY 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATAATAGTACAGCTAAATCTGTA 900

Db 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATAATAGTACAGCTAAATCTGTA 900

QY 901 GTAATTAATTGTACAAGACCCAAACAATAACAAGAAGGTTATCTATAGGACCAGGG 960  
Db |||||  
QY 961 AGAGCAATTTTATGCAAGAAGAAACATAAATAGGAGATATAAGACAAGCACATTGTAAACATT 1020  
Db |||||  
QY 1021 AGAGCAATTTTATGCAAGAAGAAACATAAATAGGAGATATAAGACAAGCACATTGTAAACATT 1020  
Db |||||  
QY 1021 AGTAGAGCAAAATGGAATAACACTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTT 1080  
Db |||||  
QY 1081 AGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTGTAATGCAC 1140  
Db |||||  
QY 1141 AGTTTAAATTGTGGAGGGGAAATCTTCTACTGTATAACAGCACAACTGTTTTAATAGTACT 1200  
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QY 1201 TGGAAATGTTACTGGAGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC 1260  
Db |||||  
QY 1261 AGAATAAAACAAATTATAAATATGTGGCAGAAAGTAGSAAAAAGCAATGTATGCCCTCCC 1320  
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QY 1321 ATCAGAGCAAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACACAGAGATGGA 1380  
Db |||||  
QY 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACTGGAGGAGGAGATATGAGGGAC 1440  
Db |||||  
QY 1441 AATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCA 1500  
Db |||||  
QY 1501 CCCACCAGGGCAAAGAGAAAGACAGTGCAAAGAGAAAAAGAGGGGCGGTTTCAGGA 1560  
Db |||||  
QY 1543 ----- 1542  
Db 1561 GGTGAGGTTCTGGAGGTGGCGGATCGGATCCAAGRAGGTTGGACAAGATAGAAGATGAA 1620  
QY 1543 ----- 1542  
Db 1621 AGGAATCTTCATGAAGATTTTGTATTTCATGAAACCGATACAGAGATGCAACACAGGAGAA 1680  
QY 1543 ----- 1542  
Db 1681 AGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAG 1740  
QY 1543 -----CCGGATCCAGNAAACAGCTTTGAAATGCAAAAAGGT 1578  
Db 1741 GATATAATGTTAAACAAGAGGAGACGAAGAAGAAAAACAGCTTTGAAATGCAAAAAGGT 1800  
QY 1579 GATCAGAATCCTCAAATTTGGGCACATGTGCATAAGTGAGGCCAGCAGTAAACACATCT 1638  
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QY 1801 GATCAGAATCCTCAAATTTGGGCACATGTGCATAAGTGAGGCCAGCAGTAAACACATCT 1860  
QY 1639 GTGTTACAGTGGGCTGAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTGGAA 1698  
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QY 1861 GTGTTACAGTGGGCTGAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTGGAA 1920  
QY 1699 AATGGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1758  
Db |||||  
QY 1921 AATGGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980

QY 1759 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAAG 1818  
Db |||||  
QY 1819 TCCCTCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 1878  
Db |||||  
QY 2041 TCCCTCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAA 2100  
QY 1879 CTTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCG 1938  
Db |||||  
QY 2101 CTTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCG 2160  
QY 1939 GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTACGTCCTTT 1998  
Db |||||  
QY 2161 GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTACGTCCTTT 2220  
QY 1999 GGCTTACTCAAACTCGAGTGATAATCTAGA 2028  
Db |||||  
QY 2221 GGCTTACTCAAACTCGAGTGATAATCTAGA 2250

RESULT 5  
ACA63265  
ID ACA63265 standard; DNA; 2046 BP.

XX ACA63265;  
XX 22-APR-2004 (first entry)  
XX HIV-1 immunogenic sequence #1.  
XX Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
XX immunogenic; virucide; ds.  
XX Human immunodeficiency virus type 1.  
XX WO2004001051-A2.  
XX 31-DEC-2003.  
XX 20-JUN-2003; 2003WO-EP007146.  
XX 20-JUN-2002; 2002EP-00291550.  
XX (INSP ) INST PASTEUR.  
XX (CNRS ) CENT NAT RECH SCI.

XX Tangy F, Lorin C, Mollet L, Delebecque F;  
XX WPI; 2004-082508/08.  
XX New recombinant mononegavirales measles virus expressing a heterologous  
PT amino acid, useful for preparing immunogenic or vaccine composition for  
PT the prophylaxis or treatment of measles.  
XX Disclosure; Fig 16A; Opp; English.

XX The present invention relates to a recombinant mononegavirales measles  
CC virus expressing a heterologous amino acid, which is capable of eliciting  
CC a humoral and/or cellular immune response against the heterologous amino  
CC acid sequence including in individuals having pre-existing measles virus  
CC immunity. The recombinant virus is useful for preparing immunogenic or  
CC vaccine composition for the prophylaxis or treatment of measles. The  
CC present sequence is a HIV immunogenic sequence shown in the  
CC exemplification of the invention

XX Sequence 2046 BP; 741 A; 328 C; 475 G; 502 T; 0 U; 0 Other;

Query Match 71.7%; Score 1453.4; DB 12; Length 2046;  
Best Local Similarity 98.3%; Pred. No. 3.7e-286;  
Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111



Db 37 TGGGGTGGAGATGGGGCACCATGCTCTTGGGATGTTGATGATCTGTAGTGTACAGAA 96  
QY 112 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA 171  
Db 97 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA 156  
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCACACAT 231  
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACAT 216  
QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGCAGAAAAAT 291  
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGCAGAAAAAT 276  
QY 292 TTTAAACATGTGGAATAAATTAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351  
Db 277 TTTAAACATGTGGAATAAATTAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336  
QY 352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCAC 411  
Db 337 GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCAC 396  
QY 412 AATTGAAATATCACTAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG 471  
Db 397 AATTGAAATATCACTAAGAACTACTACTAATCTCACTAGTAGCAGCTGGGGAATGATGGAG 456  
QY 472 AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAG 531  
Db 457 GAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAG 516  
QY 532 AAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT 591  
Db 517 AAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAGTAAAAATACTAGTAATACT 576  
QY 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTTACAGAGCCTGTCCAAAGGTATCC 651  
Db 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTTACAGAGCCTGTCCAAAGGTATCC 636  
QY 652 TTTCAGCCCAATCCCATAACATTATTGTGTCCCGCTGGGTTTGGATGCTAAAGTGTAAAC 711  
Db 637 TTTCAGCCCAATCCCATAACATTATTGTGTCCCGCTGGGTTTGGATGCTAAAGTGTAAAC 696  
QY 712 AATAAGACATTCAAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT 771  
Db 697 AATAAGACATTCAAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT 756  
QY 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 831  
Db 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 816  
QY 832 ATAGTAATTAGATCTGAAAATTTACAGACAAATGCTAAAAACCATAATAGTACAGCTAAAT 891  
Db 817 ATAGTAATTAGATCTGAAGATTTACAGACAAATGTTTAAACCATAATAGTACAGCTAAAT 876  
QY 892 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACATACAAGAAGAAGGTTATCTATA 951  
Db 877 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACATACAAGAAGAAGGTTATCTATA 936  
QY 952 GGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACAT 1011  
Db 937 GGACCAGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACAT 996  
QY 1012 TGTAACATTTAGTAGAGCAAAATGGAAATAACACTTTTACAACAGATAGTTATAAAATTAAGA 1071  
Db 997 TGTAACATTTAGTAGAGCAAAATGGAAATAACACTTTTACAACAGATAGTTATAAAATTAAGA 1056  
QY 1072 GAAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCAGAAATT 1131  
Db 1057 GAAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCAGAAATT 1116  
QY 1132 GTAATGCACAGTTTTTAATTGTGAGGGGAATTCTTCTACTGTATAACAGCAACTGTTT 1191

Db 1117 GTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAATACAGCACAACTGTTT 1176  
QY 1192 AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1251  
Db 1177 AATAGTACTTGGAAATGTTGCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA 1236  
QY 1252 CTCCAATGCAGATAAAAACAAATTTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1311  
Db 1237 CTCCAATGCAGATAAAAACAAATTTATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1296  
QY 1312 GCCCCTCCCATCAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACA 1371  
Db 1297 GCCCCTCCCATCAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACA 1356  
QY 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1431  
Db 1357 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1416  
QY 1432 ATGAGGGACAAATTGGAGAAAGTGAATTTATATAATATAAAGTAGTAAGAATTGAACCAATA 1491  
Db 1417 ATGAGGGACAAATTGGAGAAAGTGAATTTATATAAATATAAAGTAGTAAGAATTGAACCAATA 1476  
QY 1492 GGAGTAGCACCCACAGGGCAAAAGAGAAGACAGTGCAAAAGAGAAAAAGACCGG 1546  
Db 1477 GGAGTAGCACCCACAGGGCAAAAGAGAAGACAGTGCAAAAGAGAAAAAGAGCAG 1531  
RESULT 6  
ACA63266  
ID ACA63266 standard; DNA; 2610 BP.  
XX  
AC ACA63266;  
DT 22-APR-2004 (first entry)  
XX  
DE HIV-1 immunogenic sequence #2.  
XX  
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
KW immunogenic; virucide; ds.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO2004001051-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 20-JUN-2003; 2003WO-EP007146.  
XX  
PR 20-JUN-2002; 2002EP-00291550.  
XX  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
PI Tangy F, Lorin C, Mollet L, Delebecque F;  
XX  
DR WPI; 2004-082508/08.  
XX  
PT New recombinant mononegavirales measles virus expressing a heterologous  
PT amino acid, useful for preparing immunogenic or vaccine composition for  
the prophylaxis or treatment of measles.  
XX  
PS Disclosure; Fig 16C; Opp; English.  
XX  
CC The present invention relates to a recombinant mononegavirales measles  
CC virus expressing a heterologous amino acid, which is capable of eliciting  
CC a humoral and/or cellular immune response against the heterologous amino  
CC acid sequence including in individuals having pre-existing measles virus  
CC immunity. The recombinant virus is useful for preparing immunogenic or  
CC vaccine composition for the prophylaxis or treatment of measles. The  
CC present sequence is a HIV immunogenic sequence shown in the  
exemplification of the invention  
XX  
SQ Sequence 2610 BP; 885 A; 442 C; 643 G; 640 T; 0 U; 0 Other;

Query Match 71.7%; Score 1453.4; DB 12; Length 2610;  
Best Local Similarity 98.3%; Pred. No. 3.8e-286;  
Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	52	TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	37	TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	96
QY	112	AAATTGTGGGTACACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTA	171
Db	97	AAATTGTGGGTACACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTA	156
QY	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	157	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	216
QY	232	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAT	291
Db	217	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAT	276
QY	292	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351
Db	277	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	336
QY	352	GATGAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCAC	411
Db	337	GATGAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCAC	396
QY	412	AATTGGAATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	471
Db	397	AATTGGAATATCACTAAGAATACTACTAATCTCACTAGTAGCAGCTGGGGAATGATGGAG	456
QY	472	AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG	531
Db	457	GAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG	516
QY	532	AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT	591
Db	517	AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT	576
QY	592	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC	651
Db	577	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC	636
QY	652	TTTCAGCCCAATCCCATACATATTGTGTCCCGGCTGGGTTTCCGATGCTAAAGTGTAAAC	711
Db	637	TTTCAGCCCAATCCCATACATATTGTGTCCCGGCTGGGTTTCCGATGCTAAAGTGTAAAC	696
QY	712	AATAAGACATTCAATGGATCAGGACCATGACAAATGTGAGCAGCAGTACAAATGTACACAT	771
Db	697	AATAAGACATTCAATGGATCAGGACCATGACAAATGTGAGCAGCAGTACAAATGTACACAT	756
QY	772	GGAAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC	831
Db	757	GGAAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC	816
QY	832	ATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACCATAATAGTACAGCTAAAT	891
Db	817	ATAGTAATTAGATCTGAAAGATTTACAGACAATGTTAAAAACCATAATAGTACAGCTAAAT	876
QY	892	GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACATACAGAAGAGGTTTATCTATA	951
Db	877	GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACATACAGAAGAGGTTTATCTATA	936
QY	952	GGACCAGGGAGAGCATTTTATGCAAGAAGAAAAACATAATAGGAGATATAAGACAAGCACAT	1011
Db	937	GGACCAGGGAGAGCATTTTATGCAAGAAGAAAAACATAATAGGAGATATAAGACAAGCACAT	996
QY	1012	TGTPAACATTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTTATAAAATTAAAGA	1071
Db	997	TGTPAACATTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTTATAAAATTAAAGA	1056

QY	1072	GAATAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCAGAAATT	1131
Db	1057	GAATAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCAGAAATT	1116
QY	1132	GTAATGCACAGTTTTTAATTGTGGAGGGGAATTCCTTACTGTAAATACAGCACAACTGTTT	1191
Db	1117	GTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAAATACAGCACAACTGTTT	1176
QY	1192	AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA	1251
Db	1177	AATAGTACTTGGAAATGTTCTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA	1236
QY	1252	CTCCAATGCAGAATAAAACAAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT	1311
Db	1237	CTCCAATGCAGAATAAAACAAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT	1296
QY	1312	GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA	1371
Db	1297	GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACA	1356
QY	1372	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAGAT	1431
Db	1357	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAGAT	1416
QY	1432	ATGAGGGACAATTGGAGAAGTGAATTATATAATAATAAGTAGTAAGAATTGAACCAATA	1491
Db	1417	ATGAGGGACAATTGGAGAAGTGAATTATATAATAATAAGTAGTAAGAATTGAACCAATA	1476
QY	1492	GGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGACCGG	1546
Db	1477	GGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGCAG	1531

RESULT 7

AAAL56171	
ID	AAAL56171 standard; DNA; 2051 BP.
XX	
AC	AAAL56171;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	HIV truncated envelope glycoprotein 160 coding sequence.
XX	
KW	HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;
KW	gene; ds; anti-HIV; truncated.
XX	Human immunodeficiency virus.
OS	
FH	Key Location/Qualifiers
FT	CDS 1..2001
FT	/*tag= a
FT	/product= "truncated gp 160"
XX	
PN	WO2003077838-A2.
XX	
PD	25-SEP-2003.
XX	
PF	05-MAR-2002; 2002WO-US007144.
XX	
PR	05-MAR-2002; 2002WO-US007144.
XX	
PA	(NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.
XX	
PI	Dimitrov DS, Chow Y, Phogat SK, Broder CC;
XX	
DR	WPI; 2003-779074/73.
DR	P-PSDB; ABU64219.
XX	
PT	New HIV antigenic composition comprising an HIV envelope glycoprotein 160
PT	having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
PT	subunit useful for protecting a human from HIV infection.
XX	
PS	Disclosure; Page 62-63; 65pp; English.





PI	Dimitrov DS, Chow Y, Phogat SK, Broder CC;
PT	
DR	WPI; 2003-779074/73.
DR	P-PSDB; ABU64218.
XX	
PT	New HIV antigenic composition comprising an HIV envelope glycoprotein 160
PT	having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
PT	subunit useful for protecting a human from HIV infection.
XX	
PS	Disclosure; Page 61-62; 65pp; English.
XX	
CC	The present invention relates to an HIV antigenic composition, comprising
CC	an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
CC	subunit, where the carboxy-terminal end of gp120 is covalently linked
CC	through a peptide linker of at least 5 amino acids, to the amino-terminal
CC	end of gp41. The HIV antigenic composition is useful for protecting a
CC	human from HIV infection, potentially in the form of a vaccine. The
CC	present sequence is the HIV gp160 coding sequence
XX	
SQ	Sequence 2562 BP; 897 A; 433 C; 604 G; 628 T; 0 U; 0 Other;
Query Match 71.4%; Score 1447.6; DB 10; Length 2562;	
Best Local Similarity 99.2%; Pred. No. 5.7e-285;	
Matches 1466; Conservative 0; Mismatches 9; Indels 3; Gaps 1;	
QY	72 CATGCTCCTTGGGATATTGATGATCTGTAGTGCT--ACAGAAAAATTGTGGTCAAGT 128
Db	
QY	51 CTTGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAAAAGAAAAACGTGGTCAAAAT 110
Db	
QY	129 CTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATGC 188
Db	
QY	189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGA 248
Db	
QY	249 CCCAACCCACAAAGAAGTAGTATTGGGAAATGTACAGAAAAATTTTAACATGTGGAAAAA 308
Db	
QY	309 TAAATGGTGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCC 368
Db	
QY	369 ATGCTGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTCGACTAAATTTGAATATCACTAA 428
Db	
QY	429 GAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAAAA 488
Db	
QY	489 TTGCTCTTTCTATATCACCACAGCATAAGAAATAAGGTAAAGAAAGAAATATGCACTTT 548
Db	
QY	549 TAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAATAAG 608
Db	
QY	609 TTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTCAGCCCAATTCCCAT 668
Db	
QY	669 ACATTATTGTGCCGGCTGGGTTGCGATGCTAAAGTGTAAACAATAAGACATTCATGG 728
Db	
QY	729 ATCAGGACCATGCACAAATGTACAGCACAGTACAAATGTACATGGAATTAGGCCAGTGGT 788
Db	
QY	711 ATCAGGACCATGCACAAATGTACAGCACAGTACAAATGTACATGGAATTAGGCCAGTGGT 770

QY	789 GTCAAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGA 848
Db	
QY	771 GTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGA 830
Db	
QY	849 AAATTTACAGACAATGCTAAAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAATTAA 908
Db	
QY	831 AAATTTACAGACAATGCTAAAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAATTAA 890
Db	
QY	909 TTGTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCATT 968
Db	
QY	891 TTGTACAAGACCCCAACAATAACAAGAAAGGTTTATCTATAGGACCAGGGAGAGCATT 950
Db	
QY	969 TTATGCAAGAAGAAACATAATAGGAGATATAAGACAAAGCACATTTGTAACATTAGTAGAGC 1028
Db	
QY	951 TTATGCAAGAAGAAACATAATAGGAGATATAAGACAAAGCACATTTGTAACATTAGTAGAGC 1010
Db	
QY	1029 AAAATGGAATAACACTTTTACAACAGATAGTTTATAAAAATTAAAGAGAAAAAATTTAGGAATAA 1088
Db	
QY	1011 AAAATGGAATAACACTTTTACAACAGATAGTTTATAAAAATTAAAGAGAAAAAATTTAGGAATAA 1070
Db	
QY	1089 AACAAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCACAGTTTTTAA 1148
Db	
QY	1071 AACAAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCACAGTTTTTAA 1130
Db	
QY	1149 TTGTGGAGGGGAATTTCTTCTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAATGT 1208
Db	
QY	1131 TTGTGGAGGGGAATTTTCTTCTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAATGT 1190
Db	
QY	1209 TACTGGAGGGACAAATGGCACTGAAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1268
Db	
QY	1191 TACTGGAGGGACAAATGGCACTGAAAGGAAATGACATAATCACACTCCAATGCAGAAATAA 1250
Db	
QY	1269 ACAAATTATAAATATGTGSCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1328
Db	
QY	1251 ACAAATTATAAATATGTGSCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1310
Db	
QY	1329 ACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG 1388
Db	
QY	1311 ACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAG 1370
Db	
QY	1389 TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTTGGAG 1448
Db	
QY	1371 TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTTGGAG 1430
Db	
QY	1449 AAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAG 1508
Db	
QY	1431 AAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAG 1490
Db	
QY	1509 GGCAAAAGAGAGAAACAGTGCAAAAGAGAAAAAAGACCGG 1546
Db	
QY	1491 GGCAAAAGAGAGAAACAGTGCAAAAGAGAAAAAAGAGCAG 1528
Db	
RESULT 9	
ACA63267	
ID	ACA63267 standard; DNA; 2010 BP.
XX	
AC	ACA63267;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	HIV-1 immunogenic sequence #3.
XX	
KW	Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;
KW	immunogenic; virucide; ds.
OS	Human immunodeficiency virus type 1.
XX	
PN	WO2004001051-A2.
XX	
PD	31-DEC-2003.
XX	
PF	20-JUN-2003; 2003WO-EP007146.

XX PR 20-JUN-2002; 2002EP-00291550.  
XX (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
XX Tangy F, Lorin C, Mollet L, Delebecque F;  
XX WPI; 2004-082508/08.  
XX  
PT New recombinant mononegavirales measles virus expressing a heterologous  
PT amino acid, useful for preparing immunogenic or vaccine composition for  
PT the prophylaxis or treatment of measles.  
XX  
XX Disclosure; Fig 16E; Opp; English.  
XX  
CC The present invention relates to a recombinant mononegavirales measles  
CC virus expressing a heterologous amino acid, which is capable of eliciting  
CC a humoral and/or cellular immune response against the heterologous amino  
CC acid sequence including in individuals having pre-existing measles virus  
CC immunity. The recombinant virus is useful for preparing immunogenic or  
CC vaccine composition for the prophylaxis or treatment of measles. The  
CC present sequence is a HIV immunogenic sequence shown in the  
CC exemplification of the invention  
XX  
SQ Sequence 2010 BP; 720 A; 326 C; 469 G; 495 T; 0 U; 0 Other;  
Query Match 66.0%; Score 1339.4; DB 12; Length 2010;  
Best Local Similarity 94.5%; Pred. No. 5.8e-263;  
Matches 1413; Conservative 0; Mismatches 46; Indels 36; Gaps 1;  
QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111  
DB 37 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 96  
QY 112 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171  
DB 97 AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 156  
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231  
DB 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216  
QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTACAGAAAAAT 291  
DB 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTACAGAAAAAT 276  
QY 292 TTTTAAATGTGGAATAAACAATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351  
DB 277 TTTTAAATGTGGAATAAACAATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336  
QY 352 GATGAAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT 411  
DB 337 GATGAAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTACTTTAAATTTGCACT 396  
QY 412 AATTGGAATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG 471  
DB 397 AATTGGAATATCACTAAGAATACTACTAATCTCACTAGTAGCAGCTGGGGAATGATGGAG 456  
QY 472 AAAGGAGAAAAATAAAAAATTGCTCTTTCTATATCACCACAGCATAAGAAATAAGGTAAAG 531  
DB 457 GAAGGAGAAAAATAAAAAATTGCTCTTCTATATCACCACAGCATAAGAAATAAGGTAAAG 516  
QY 532 AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACT 591  
DB 517 AAAGAATATGCACCTTTTAAATAGACTTGATGTAGTACCAGTAAAAATACTAGTAATACT 576  
QY 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC 651  
DB 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCC 636  
QY 652 TTTCAGCCAATTCCCATACATTATTGTGTCGGCTGGGTTTGGGATGCTAAAGTGTAAAC 711

DB 637 TTTCAGCCAAATCCCATAPACATTATTGTGTCCCGGTGGGTTTGGATACTAAAGTGTAAAC 696  
QY 712 AATAAGACATTCATGGATCAGGACCATGCACAATGTTCAGCACAGTACAATGTACACAT 771  
DB 697 AATAAGACATTCATGGATCAGGACCATGCACAATGTTCAGCACAGTACAATGTACACAT 756  
QY 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAAATGGCAGTCTAGCAGAAAGAGAC 831  
DB 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAAATGGCAGTCTAGCAGAAAGAGAC 816  
QY 832 ATAGTAATTAGATCTGAAAAATTTTCACAGACAATGTCTAAAACCATATAATAGTACAGCTAAAT 891  
DB 817 ATAGTAATTAGATCTGAAAGATTTTCACAGACAATGTCTAAAACCATATAATAGTACAGCTAAAT 876  
QY 892 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTATCTATA 951  
DB 877 GAATCTGTAGTAATTAAATTGTACAAGACCCCAACAACAATGC----- 917  
QY 952 GGACCAGGGAGAGCAATTTTATGCAAGAAGAAACAATAATAGGAGATATAAGACAAAGCACAT 1011  
DB 918 -----TGCAGAAATTGGATAAAATGGCAAGTGTCTGCAAGACAAAGCACAT 960  
QY 1012 TGTAAACATTAGTAGAGCAAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTTAAGA 1071  
DB 961 TGTAAACATTAGTAGAGCAAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTTAAGA 1020  
QY 1072 GAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATT 1131  
DB 1021 GAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATT 1080  
QY 1132 GTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTACTGTAAATACAGCACAACTGTTT 1191  
DB 1081 GTAATGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAAATACAGCACAACTGTTT 1140  
QY 1192 AATAGTACTTGGAAATGTTACTGGAGGGACAAAATGGCACTGAAGGAAATGACATAATCACA 1251  
DB 1141 AATAGTACTTGGAAATGTTCTGGAGGGACAAAATGGCACTGAAGGAAATGACATAATCACA 1200  
QY 1252 CTCCAATGCAGAAATAAACAAAATTATAAATATGTGGCAGAAAAAGTAGGAAAAGCAATGTAT 1311  
DB 1201 CTCCAATGCAGAAATAAACAAAATTATAAATATGTGGCAGAAAAAGTAGGAAAAGCAATGTAT 1260  
QY 1312 GCCCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAACA 1371  
DB 1261 GCCCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAACA 1320  
QY 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431  
DB 1321 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1380  
QY 1432 ATGAGGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATA 1491  
DB 1381 ATGAGGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATA 1440  
QY 1492 GGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGACCGG 1546  
DB 1441 GGAGTAGCACCCACCAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGCAG 1495  
RESULT 10  
ACA63268  
ID ACA63268 standard; DNA; 2574 BP.  
XX  
AC ACA63268;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE HIV-1 immunogenic sequence #4.  
XX  
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;  
KW immunogenic; virucide; ds.  
XX  
OS Human immunodeficiency virus type 1.





XX Env gene of the BA-L strain of Human immunodeficiency virus type 1.

DE HIV-1; HIV-1 strain BA-L; env protein; vaccine; immunotherapy;

XX HIV infection; immunogen; HIV-1 diagnosis; ds.

KW Human immunodeficiency virus 1.

XX

OS

XX

FH Key Location/Qualifiers

FT CDS 648..3214

FT /\*tag= a

FT /product= "env\_protein"

FT /transl\_except= (pos: 678..678, aa: Gln)

XX

PN US5869313-A.

XX

PD 09-FEB-1999.

XX

PF 14-MAY-1996; 96US-00647714.

XX

PR 17-OCT-1990; 90US-00599491.

PR 25-FEB-1993; 93US-00022835.

PR 15-FEB-1995; 95US-00388809.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Gallo RC, Franchini G, Reitz MS, Lori FC, Popovic M, Gartner S; Markham PD;

XX

DR WPI; 1999-152779/13.

DR P-PSDB; AAW88113.

XX

PT DNA encoding env protein of the human immune deficiency virus isolate BA-L - useful for producing protein for use in vaccines, as assay reagent and to generate antibodies.

XX

PS Claim 2; Fig 8A-H; 87pp; English.

XX

CC The present sequence encodes the envelope protein of the BA-L (ATCC 40890) strain of Human immunodeficiency virus type 1 (HIV-1) strain MN-ST1. BA-L is more typical of United States isolates of HIV-1 than previously known strains. Recombinant, complete env protein of the BA-L strain is used as a vaccine component and for immunotherapy of existing HIV infections, to detect HIV-specific antibodies, e.g. in donated blood, and as an immunogen to raise specific antibodies, for HIV-1 diagnosis. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 3806 BP; 1306 A; 662 C; 937 G; 901 T; 0 U; 0 Other;

Query Match 60.4%; Score 1225.4; DB 2; Length 3806;

Best Local Similarity 90.2%; Pred. No. 9.9e-240;

Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGGGTCACAGTCTA 131

DB 700 CATGCTCCTTGGGATATTAAATGATCTGTAATGCTGAAGAAAAATTGTGGGTCACAGTCTA 759

QY 132 TTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGCTAA 191

DB 760 TTATGGGGTACCTGTGTGGAAAGAAGCAACCACCTCTATTTTGTGCATCAGATCCTAA 819

QY 192 AGCCTATGATACAGAGGTACATAAATGTTTGGCCACACATGCTGTGTACCCACAGACCC 251

DB 820 AGCATATGATACAGAGGTACATAAATGTTTGGCCACACATGCTGTGTACCCACAGACCC 879

QY 252 CAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGGAAAAATAA 311

DB 880 CAACCCACAAGAAGTAGAATTGAAAAAATGTGACAGAAAAATTTAAACATGTGGAAAAATAA 939

QY 312 CATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCCATG 371

DB 940 CATGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCCCTAAAGCCATG 999

QY 372 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACTAAATTGA-----ATATCAC 425

DB 1000 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACTGATTTGAGGAATGCTACTAA 1059

QY 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAA 485

DB 1060 TGGGAATGACACTAATACCACCTAGTAGTAGCAGGGGAATGGTGGGGGAGGAGAAATGAA 1119

QY 486 AAATTGCTCTTTCTATATCACCAAGCATAAGAAATAAGGTAAAGAAAGAAATATGCACT 545

DB 1120 AAATTGCTCTTTCAATATCACCAACAACATAAGAGGTAAGGTGCAGAAAGAATATGCACT 1179

QY 546 TTTTAAATAGACTTGATGTAGTACCACCAATAGAAAAATACTAATAACTAAAGTATAGGTTAAT 605

DB 1180 TTTTATAAAACCTTGATATAGCACCAATAGATAATAATAGTAATAATAGATATAGGTTGAT 1239

QY 606 AAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAAATTCC 665

DB 1240 AAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCAAATTCC 1299

QY 666 CATACATATTGTGCCGGCTGGGTTTTCGATGCTAAAGTGTAAAGTGTAAACAATAAGACATTCAA 725

DB 1300 CATACATATTGTGCCGGCTGGGTTTTCGATGCTAAAGTGTAAAGTGTAAAGATAAGAAGTTCAA 1359

QY 726 TGGATCAGGACCATGCACAAAATGTGAGCAGACAGTACAATGTACACATGGAATTAGGCCAGT 785

DB 1360 TGGAAAAGGACCATGTACAAAATGTGAGCAGACAGTACAATGTACACATGGAATTAGGCCAGT 1419

QY 786 GGTGTCAACTCAACTGCTGTAAATGGCAGCTCTAGCAGAAAGACATAGTAATTAGATC 845

DB 1420 AGTATCAACTCAACTGCTGTAAATGGCAGCTCTAGCAGAAAGAGGTTAGTAATTAGATC 1479

QY 846 TGAAAAATTTTCACAGACCAATGCTAAAAACCATATAATAGTACAGCTAAATGAATCTGTAGTAAT 905

DB 1480 CGCCAAATTTCCGGACAATGCTAAAGTCAATAATAGTACAGCTGAATGAATCTGTAGAAAT 1539

QY 906 TAATTGTACAAGACCCCAACAACATAACAAGAAAGGTTATCTATAGGACCAGGAGAGC 965

DB 1540 TAATTGTACAAGACCCCAACAACATAACAAGAAAAAGTATACATATAGGACCAGGAGAGC 1599

QY 966 ATTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG 1025

DB 1600 ATTTTATACAACAGGAGAAAAATAATAGGAGATATAAGACAAGCACATTGTAACCTTAGTAG 1659

QY 1026 AGCAAAATGGAATAACACTTTACAACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAA 1085

DB 1660 AGCAAAATGGAATGACACTTTAAATAAGATAGTTATATAAAATTAAGAGAACAAATTTGGGAA 1719

QY 1086 TAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTT 1145

DB 1720 TAAAACAATAGTCTTTAAGCACTCCTCAGGAGGGGACCCAGAAATTTGTGACGCACAGTTT 1779

QY 1146 TAATTGTGGAGGGGAATTTCTTACTGTAAATACAGCAAACTGTTTAAATAGTACTTTGGAA 1205

DB 1780 TAATTGTGGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAAATAGTACTTTGGAA 1839

QY 1206 TGTTACTGGAGGGACAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAAT 1265

DB 1840 TGTTACTGAAGAGTCAATAAACAACACTGTAGAAAAATAACAACAATCACACTCCCATGCAGAAAT 1899

QY 1266 AAAACAAATTTATAAATATGTGGCAGAAAAGTAGGAAAAAGCAATGTATGCCCTCCCAATCAC 1325

DB 1900 AAAACAAATTTATAAACAATGTGGCAGGAAGTAGGAAAGAGCAATGTATGCCCTCCCAATCAC 1959

QY 1326 AGGACAAATTTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGTAA 1385

DB 1960 AGGACAAATTTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG-- 2016

QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAAATTG 1445

DB 2017 TCCTGAGGACAAACAAGACCGAGGTCTTCAGACCTGGAGGAGAGATATGAGGGGATAATTG 2076

QY 1446 GAGAAGTGAATTATATAAATATAAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCAC 1505



Db 1781 TAATTGTGGAGGGGAATTTTCTACTGTAAATTCACACAACACTGTTTAAATAGTACTTGGAA 1840

QY 1206 TGTTACTGGAGGACAAATGGCACTGAAGGAAATGACATAAATCACACTCCAATGCAGAAT 1265

Db 1841 TGTTACTGAAGAGTCAAATAACACTGTAGAAAATAACACAATCACACTCCCATGCAGAAT 1900

QY 1266 AAAACAAATTATAAATATGTGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1325

Db 1901 AAAACAAATTATAACATGTGCAGGAAGTAGGAAGGCAATGTATGCCCTCCCATCAG 1960

QY 1326 AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAAGAGATGGAGGTAA 1385

Db 1961 AGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--- 2017

QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 1445

Db 2018 TCCTGAGGACAACAAGACCGAGTCTTCAGACCTGGAGGAGGAGATATGAGGGATAATTG 2077

QY 1446 GAGAAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAAACCAATAGGAGTAGCACCCAC 1505

Db 2078 GAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAAACCATTAGGAGTAGCACCCAC 2137

QY 1506 CAGGGCAAAGAGAAGAACAGTGTCAAAAGAGAAAAAGACCGG 1546

Db 2138 CAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAG 2178

RESULT 13

ADO52562

ID ADO52562 standard; DNA; 9540 BP.

XX

AC ADO52562;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human immunodeficiency virus 1 parent JRCSF DNA.

XX

KW Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy;

KW vaccine; ds.

XX

OS Human immunodeficiency virus 1.

XX

PN US2004101823-A1.

XX

PD 27-MAY-2004.

XX

PF 19-DEC-2002; 2002US-00325468.

XX

PR 21-DEC-2001; 2001US-0343524P.

XX

PA (MAXY-) MAXYGEN INC.

XX

PI Soong NW, Pekrun K, Shibata R;

XX

DR WPI; 2004-399670/37.

XX

DR GENBANK; M38429.

PT New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a

PT composition for treating or preventing infection caused by HIV-1.

XX

PS Disclosure; SEQ ID NO 46; 310pp; English.

XX

CC The present invention relates to human immunodeficiency virus 1 (HIV-1)

CC viral variants and nucleic acids and polypeptides thereof having improved

CC replication properties for development of suitable animal models for the

CC study of HIV-1 pathogenesis. The invention is useful for treating and

CC preventing HIV-1 infection. The invention is also useful in gene therapy

CC and in the preparation of vaccines. The present sequence is human

CC immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the

XX invention.

Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 60.2%; Score 1221.8; DB 12; Length 9540;

Best Local Similarity 90.4%; Pred. No. 6e-239;

Matches 1333; Conservative 0; Mismatches 127; Indels 15; Gaps 2;

QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTGTGGTCCAGTCTA 131

Db 6289 CTTGCTCCTTGGGACATTAAATGATCTGTAGTGTCTAGAAAAAGTTGTGGTCCAGTCTA 6348

QY 132 TTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAA 191

Db 6349 TTATGGGGTACCTGTGTGGAAAGAAACAACCACCACTCTATTTTGTGCATCAGATGCTAA 6408

QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251

Db 6409 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 6468

QY 252 CAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGGAAAAATAA 311

Db 6469 CAACCCACAAGAGTAGTATTGGAAAAATGTAAACAAGATTTTAAACATGTGGAAAAATAA 6528

QY 312 CATGGTAGATCAGATGAGGATATAAATCAGTTTATGGGATGAAAGCCTAAAGCCATG 371

Db 6529 CATGGTAGAACAGATGCAGGAGGATGTAATCAATTTATGGGATCAAAGCTTAAAGCCATG 6588

QY 372 TGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTCGACTAAATTTGAATATCACTAAGAA 431

Db 6589 TGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTCGAAAAGATGT-----GAA 6636

QY 432 TACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAGAAAAGGAGAAATAAAAAATTG 491

Db 6637 TGCTACTAATACCACCTAGTAGTAGTGAGGGAATGATGGAGAGAGGAGAAATAAAAAACTG 6696

QY 492 CTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAGAAAGAATATGCACITTTTAA 551

Db 6697 CTCTTTCAATATCACCCAAAGCATAAGAGATAAGGTGCAGAAAGAATATGCTCTTTTAA 6756

QY 552 TAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTAATAAGTTG 611

Db 6757 TAAACTGGATGTAGTACCAATAGATAATAAGAAATAACCAAAATATAGGTTAATAAGTTG 6816

QY 612 TAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTAGCCCAATCCCATACA 671

Db 6817 TAACACCTCAGTCATTACACAAGCCTGTCCAAAGGTATCCTTTGAACCAATTCCTCCATACA 6876

QY 672 TTATTGTGTCCCGGTGGTTTTCGATGTCTAAAAGTGAACAATAAGACATTCATGGATC 731

Db 6877 TTATTGTGCCCCGGCTGGTTTTCGGAATTCCTAAAAGTGAATAATAAGACATTCATGGAAA 6936

QY 732 AGGACCATGCACAAATGTGCAGCACAGTACAATGTACATGGAATTAGGCCAGTGGTGTG 791

Db 6937 AGGACAATGTAAAAATGTGCAGCACAGTACAATGTACATGGAATTAGGCCAGTAGTATC 6996

QY 792 AACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAAAGACATAGTAATTAGATCTGAAA 851

Db 6997 AACTCAACTGCTGCTAAATGGCAGTCTAGCAGAAGAAAGGTTGTAATTAGATCTGACAA 7056

QY 852 TTTACAGACAAATGCTAAAAACCATAATAGTACAGCTTAAATGAATCTGTAGTAATTATTG 911

Db 7057 TTTACGGACAAATGCTAAAAACCATAATAGTACAGCTGAATGAATCTGTAAAAATTAATTG 7116

QY 912 TACAAGACCCCAACAATAFACAAAGAAAGGTTTATCTATAGGACCAGGGAGAGCATTTTA 971

Db 7117 TACAAGGCCAGCAACAATAFACAAAGAAAAAGTATACATATAGGACCAGGGAGAGCATTTTA 7176

QY 972 TGCAAGAAGAAACATAATAGGAGATATAAGCAAGCAACATGTAACATTAGTAGAGCAAA 1031

Db 7177 TACAACAGGAGAAATAATAGGAGATATAAGACAAGCAATGTAACATTAGTAGAGCACA 7236

QY 1032 ATGGAATAACACTTTTACAACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAATAAAC 1091

Db 7237 ATGGAATAACACTTTTAAACAGATAGTTTGAAAAAATTAAGAGAACAAATTTAATAATAAAC 7296

QY 1092 AATAGCCTTTAATCAATCCTCAGGAGGGGCCAGGAAATTTAATGCACAGTTTAAATTG 1151



Db 7297 AATAGTCTTTACTCACTCCTCAGAGGGGATCCAGAAATTGTAATGCACAGTTTAAATG 7356  
Qy 1152 TGGAGGGGAATCTTCTACTGTGTAATACAGCACAACTGTTTAATAGTACTTGGAAATGTTAC 1211  
Db 7357 TGGAGGGGAATTTTCTACTGTGTAATCAACACAACTGTTTAATAGTACTTGGAAATGATAC 7416  
Qy 1212 TGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACTCCAATGCAGAAATAAACA 1271  
Db 7417 TGAAGAGTCAAGTGGCACTGAAGGAAATGACACCATCATCTCCCATGCAGAAATAAACA 7476  
Qy 1272 AATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGGACA 1331  
Db 7477 AATTATAACATGTGGCAGGAAGTGGGAAAAGCAATGTATGCTCTCCCATTAAGGACA 7536  
Qy 1332 AATTAGATGTTCAATCAATATTACAGGGCTGCTACTAAAGAGATGGAGGTAATAGTAC 1391  
Db 7537 AATTAGATGTTCAATCAATATTACAGGGCTGCTATTAAAGAGATGGTGGTAA---AAA 7593  
Qy 1392 TGAGACTGAGACTGAGATCTTCAGACCTTGAGGAGGAGATATGAGGGACAATTTGGAGAAG 1451  
Db 7594 TGAGAGTGAGATCGAGATCTTCAGACCTTGAGGAGGAGACATGAGGGACAATTTGGAGAAG 7653  
Qy 1452 TGAATTATATAAATATAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCACCAAGGC 1511  
Db 7654 TGAATTATATAAATATAAAGTAGTAAGAAAATTGAACCAATTAGGAGTAGCACCCACCAAGGC 7713  
Qy 1512 AAAGAGAAGAACAGTGCAAGAGAGAAAAAGACCGG 1546  
Db 7714 AAAGAGAAGAGTGGTGCAAGAGAGAAAAAGAGCAG 7748  
RESULT 14  
ADP20074  
ID ADP20074 standard; DNA; 9540 BP.  
XX AC ADP20074;  
XX DT 09-SEP-2004 (first entry)  
XX DE Human immunodeficiency virus 1 isolate JRCSF nucleotide sequence.  
KW immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;  
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;  
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSF;  
KW gene; ds.  
XX OS Human immunodeficiency virus 1.  
XX FH Key Location/Qualifiers  
FT LTR 1. .635  
FT partial  
FT CDS 790. .2304  
FT \*tag= a  
FT \*tag= b  
FT /product= "gag"  
FT 2085. .5108  
FT \*tag= c  
FT /product= "pol"  
FT 5053. .5631  
FT \*tag= d  
FT /product= "vif"  
FT 5571. .5861  
FT \*tag= e  
FT /product= "vpr"  
FT 6073. .6318  
FT \*tag= f  
FT /product= "vpu"  
FT 6236. .8782  
FT \*tag= g  
FT /product= "env"  
FT 8784. .9434  
FT \*tag= h

FT /product= "nef"  
FT 9103. .9540  
FT \*tag= i  
XX partial  
PN WO2004053100-A2.  
XX 24-JUN-2004.  
XX 11-DEC-2003; 2003WO-US039534.  
PR 11-DEC-2002; 2002US-0432869P.  
PR 24-APR-2003; 2003US-0465350P.  
XX (SCRI ) SCRIPPS RES INST.  
XX Burton DR, Wilson I, Pantophlet R;  
PI WPI; 2004-480933/45.  
XX P-PSDB; ADP20067, ADP20068, ADP20069, ADP20070, ADP20071, ADP20072,  
DR ADP20073.  
DR GENBANK; M38429.  
XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against  
PT the polypeptide, useful preventing or treating human immunodeficiency  
PT virus (HIV) infection, especially HIV-1 infection.  
XX PS Disclosure; Page 139-141; 149pp; English.  
XX CC The present invention describes an immunogenic mutant HIV gp120  
CC polypeptide that can stimulate a neutralising antibody response against a  
CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic  
CC mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising  
CC antibody response against a panel of HIV-1 comprising HIV-1 primary  
CC isolates of at least two different clades, where the mutant gp120 has at  
CC least one amino acid mutation in at least one epitope of the HIV-1 gp120  
CC polypeptide specifically bound by a neutralising antibody, which reduces  
CC binding affinity of the non-neutralising antibody; (2) an immunogenic  
CC mutant HIV-1 gp120 polypeptide (Ib) having at least one amino acid  
CC mutation in at least one epitope of the gp120 polypeptide specifically  
CC bound by a non-neutralising antibody; (3) a vaccine (II) comprising one  
CC or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5)  
CC an isolated HIV neutralising antibody (IV) fraction obtained by using  
CC (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V)  
CC obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in  
CC a subject, by administering an HIV neutralising antibody produced in  
CC response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV  
CC -1 infection in a human subject, involves administering HIV-1  
CC neutralising antibodies to the subject, where the HIV-1 neutralising  
CC antibodies comprise antibodies stimulated in response to (II); (9) HIV  
CC neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV  
CC neutralising antibodies (VII) obtained by using (Ib); and (11) isolated  
CC HIV-1 neutralising antibodies obtained by harvesting spleen and lymph  
CC nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV  
CC activities, and can be used in vaccines and in HIV binding agents. (Ia)  
CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1  
CC which involves immunising a subject with a (Ia) or (Ib). The antibodies  
CC are useful for preventing or ameliorating HIV, especially HIV-1,  
CC infection in a subject. The present sequence represents an HIV-1 isolate  
CC JRCSF genomic nucleotide sequence, which is given in the exemplification  
XX of the present invention.  
SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;  
Query Match 60.2%; Score 1221.8; DB 12; Length 9540;  
Best Local Similarity 90.4%; Pred. No. 6e-239;  
Matches 1333; Conservative 0; Mismatches 127; Indels 15; Gaps 2;  
Qy 72 CATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGGTCAAGTCTA 131  
Db 6289 CTTGCTCCTTGGGACATTAATGATCTGTAGTGTAGAAAAAGTTGTGGTCAAGTCTA 6348  
Qy 132 TTATGGGGTACCTGTGTGGAGAGAGCAACCACTACTCTATTTTGTGCATCAGATGCTAA 191



CC using a HIV-1 envelope probe. This clone, designated BA-L1, contained the  
CC entire env gene. The insert was subcloned and sequenced. The BA-L plasmid  
CC clone has been deposited as ATCC 40890. The sequence also contains the  
CC coding region for the rev protein which is needed for efficient  
CC expression of the envelope protein in eukaryotic cells. (Note: Revised  
CC entry submitted to correct the patent number format of US Government-  
CC owned NTIS applications to prevent clashes with ongoing US granted patent  
CC numbers. For further information please visit the Derwent web site at  
CC www.derwent.com/dwpi/updates/ntis\_us.html.) (Updated on 25-MAR-2003 to  
CC correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)  
XX

SQ Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;

Query Match 60.1%; Score 1219; DB 2; Length 3807;  
Best Local Similarity 89.9%; Pred. No. 2e-238;  
Matches 1332; Conservative 0; Mismatches 140; Indels 9; Gaps 2;

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QY	132	TTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGTGCATCAGATGCTAA	191
Db	761	TTATGGGTTACCTGTGTGGAAGAAGCAACCACCTCTATTTTGTGCATCAGATCGTAA	820
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QY	312	CATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCCATG	371
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Db	1001	TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATGTTTGAGGAATGCTACTAA	1060
QY	426	TAAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAATAA	485
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Db	1121	AAATTGCTCTTTCAATATACCAACAACATAGAGGTTAAGGTGCAGAAAGATATGCACCT	1180
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Db	1241	AAGTTGTAACACCTCAGTCATTAACACAGGCCTGTCCAAAGGTATCCTTTTGAGCCAATTCC	1300
QY	666	CATACATATTGTGTCCCGCTGGGTTTTCGATGCTTAAAGTGTAAACAATAAGACATTCAA	725
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QY	786	GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAAGACATAGTAATTAGATC	845
Db	1421	AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAAGAGGTAGTAATTAGATC	1480
QY	846	TGAAAAATTTACAGACAAATGCTAAAAACCATAATAATAGTACAGCTAAATGAATCTGTAGTAAT	905
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Db	2138	CAAGGCAAAGAGAGAGTGGTGCAGAGAGAGAAAAAAGAGCAG	2178

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1225.4	60.4	3807	1 US-08-388-809-5	Sequence 5, Appli
3	1225.4	60.4	3807	2 US-08-647-714-5	Sequence 5, Appli
C 4	1174.2	57.9	3807	2 US-08-417-210A-78	Sequence 78, Appli
C 5	1174.2	57.9	3807	4 US-09-136-159A-78	Sequence 78, Appli
6	1172.6	57.8	2552	2 US-08-448-603A-27	Sequence 27, Appli
7	1172.6	57.8	2552	3 US-09-134-075-27	Sequence 27, Appli
8	1172.6	57.8	2552	3 US-09-492-739-27	Sequence 27, Appli
9	1172.2	57.8	2571	1 US-08-254-358-3	Sequence 3, Appli
10	1172.2	57.8	2571	1 US-08-475-391-3	Sequence 3, Appli
11	1172.2	57.8	2571	2 US-08-709-609-3	Sequence 3, Appli
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13	1172.2	57.8	2571	4 US-09-936-572-3	Sequence 3, Appli
14	1172.2	57.8	2571	5 PCT-US95-07178-3	Sequence 3, Appli
C 15	1172.2	57.8	6474	3 US-08-651-472-66	Sequence 66, Appli
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26	1171.4	57.8	1539	3 US-08-472-240A-13	Sequence 13, Appli
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39	1161.2	57.3	2570	3 US-09-134-075-31	Sequence 31, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 5, Application US/08022835  
; Patent No. 5420030  
; GENERAL INFORMATION:  
; APPLICANT: Reitz Jr., Marvin S.  
; APPLICANT: Franchini, Genoveffa  
; APPLICANT: Markham, Phillip D.  
; APPLICANT: Gallo, Robert C.  
; APPLICANT: Lori, Franco C.  
; APPLICANT: Popovic, Mikulas  
; APPLICANT: Garnter, Suzanne  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/022,835  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scott, Watson T.  
; REGISTRATION NUMBER: 26,581  
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3807 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: 648..3215									
US-08-022-835-5									
Query Match 60.4%; Score 1225.4; DB 1; Length 3807;									
Best Local Similarity 90.2%; Pred. No. 8.3e-305;									
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;									
QY	72	CATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGGGTCAAGTCTTA	131						
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QY	1026	AGCAAAATGGAATAACACTTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAA	1085						

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QY	1206	TGTTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAAT	1265
Db	1841	TGTTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACACAATCACACTCCCATGCAGAAAT	1900
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QY	1326	AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAACAAAGAGATGGAGGTAA	1385
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RESULT 2

US-08-388-809-5  
; Sequence 5, Application US/08388809  
; Patent No. 5576000  
; GENERAL INFORMATION:  
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT  
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
; APPLICANT: GARTNER, SUZANNE  
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK, 3.5"  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,809  
; FILING DATE: 15-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,835  
; FILING DATE: 25-FEB-1993  
; APPLICATION NUMBER: US 07/599,491  
; FILING DATE: 17-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LESLIE A. SERUNIAN  
; REGISTRATION NUMBER: 35,353  
; REFERENCE/DOCKET NUMBER: 2026-4092US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800



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; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3215
US-08-388-809-5

Query Match      60.4%; Score 1225.4; DB 1; Length 3807;
Best Local Similarity 90.2%; Pred. No. 8.3e-305;
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Db 1241 AAGTTGTAACACCTCAGTCAATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATTCC 1300

QY 666 CATACATTATTGTGTCGCCGCTGGGTTTTCGATGCTTAAAGTGTAAACAATAAGACATTCAA 725
Db 1301 CATACATTATTGTGCCCGCTGGTTTTTCGATTTCTAAAGTGTAAAGATAAGAAAGTTCAA 1360

QY 726 TGGATCAGGACCATGCACAAATGTTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT 785
Db 1361 TGGAAAAGGACCATGTACAAATGTTCAGCACAGTACAATGTACACATGGAATTAGGCCAGT 1420

QY 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATC 845
Db 1421 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATC 1480

QY 846 TGAATAATTTACAGACAATGCTTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT 905
Db 1481 CGCCAATTTTCGGGACAAATGCTTAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540
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QY 906 TAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGAGC 965
Db 1541 TAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATACATATAGGACCAGGCAGC 1600

QY 966 ATTTTATGCAAGAAAGAACATATAATAGGAGATATAAGACAAGCACATTGTAACTTAGTAG 1025
Db 1601 ATTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACTTAGTAG 1660

QY 1026 AGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAA 1085
Db 1661 AGCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTAAGAGAAACAATTTGGGAA 1720

QY 1086 TAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAAATTTGTAATGCACAGTTT 1145
Db 1721 TAAAACAATAGTCTTTTAAAGCACTCCTCAGGAGGGGACCCAGAAAAATTTGACGCACAGTTT 1780

QY 1146 TAATTGTGAGGGGAATTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTTGGAA 1205
Db 1781 TAATTGTGAGGGGAATTCTTCTACTGTAATTCACAACAACCTGTTTAAATAGTACTTTGGAA 1840

QY 1206 TGTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGCAGAAAT 1265
Db 1841 TGTACTGAAGAGTCAATAACACTGTAGAAAAATAACACAATCACACTCCCCATGCAGAAAT 1900

QY 1266 AAAACAAATTATTAATATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCCCTCCCATCAC 1325
Db 1901 AAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAGAGCAATGTATGCCCCCTCCCATCAG 1960

QY 1326 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAA 1385
Db 1961 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--- 2017

QY 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGAGATATGAGGGACAATTTG 1445
Db 2018 TCCTGAGGACAACAAGACCGAGGTCTTCAGACCTCGAGGAGGAGATATGAGGGATAATTG 2077

QY 1446 GAGAAAGTGAATTATATAAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCAC 1505
Db 2078 GAGAAAGTGAATTATATAAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCAC 2137

QY 1506 CAGGGCAAAGAGAGAACACAGTGCAAAGAGAGAAAAAGACCCGG 1546
Db 2138 CAAGGCAAAGAGAGAGAGTGGTGCAGAGAGAGAAAAAGAGCAG 2178
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RESULT 3
US-08-647-714-5
; Sequence 5, Application US/08647714
; Patent No. 5869313
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,714
; FILING DATE:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/388,809
; FILING DATE: 15-FEB-1995
; APPLICATION NUMBER: US 08/022,835
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: LESLIE A. SERUNIAN
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4092US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3215
;
US-08-647-714-5

Query Match          60.4%; Score 1225.4; DB 2; Length 3807;
Best Local Similarity 90.2%; Pred. No. 8.3e-305;
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

QY 72 CATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAAATTGTGGGTCACAGTCTA 131
Db 701 CATGCTCCTTGGGATATTGATGATCTGTAATGCTGAAGAAAAATTGTGGGTCACAGTCTA 760

QY 132 TTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCATCAGATGCTAA 191
Db 761 TTATGGGGTACCTGTGTGGAAAGAACCAACCACCTCTATTTTGTGCATCAGATCGTAA 820

QY 192 AGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251
Db 821 AGCATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 880

QY 252 CAACCCACAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA 311
Db 881 CAACCCACAAGAAAGTAGAATTGAAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA 940

QY 312 CATGTPAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCCATG 371
Db 941 CATGTPAGAACAATGTCATGAGGATATAATCAGTTTATGGGATCAAAGCCCTAAAGCCATG 1000

QY 372 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACCTAATTTGA-----ATATCAC 425
Db 1001 TGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACCTGATTTGAGGAATGCTIATAA 1060

QY 426 TAAGAACTACTACTAATCCCACCTAGTAGCAGCTGGGGATGATGGAGAAAAGGAGAAATAAA 485
Db 1061 TGGGAATGACACTAATACCACTAGTAGTAGCAGGGGAAATGGTGGGGGAGGAGAAATGAA 1120

QY 486 AAATTGCTCTTTCTATATACCAAGCATATAAGAAATAAGGTAAGAAAGAAAGAAATATGCAC 545
Db 1121 AAATTGCTCTTTCAATATATCACCAAAACATAAGAGGTAAGGTGAGAGAAAGAAATATGCAC 1180

QY 546 TTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGGTTAAT 605
Db 1181 TTTTATAAACTTGATATAGCACCAATAGATAATAATAGTAATAATAGATATAGGTTGAT 1240

QY 606 AAGTTGTAACACCTCAGTCATTACAGAGCCCTGTCCAAAGGTATCCTTTTCAGCCAATTCC 665
Db 1241 AAGTTGTAACACCTCAGTCATTACAGAGCCCTGTCCAAAGGTATCCTTTTGAGCCAATTCC 1300

QY 666 CATACATTTATTGTGTCCCGGCTGGGTTTGCATGCTAAAGTGTAAACAATAAGACATTTCAA 725
Db 1301 CATACATTTATTGTGTCCCGGCTGGGTTTTCGATTCTTAAAGTGTAAAGATAAGAAGTTCAA 1360
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QY 726 TGGATCAGGACCATGCACAAAATGTCCAGCACAGTACAAATGTACACATGGAAATTAGCCAGT 785
Db 1361 TGGAAAAGGACCATGTACAAAATGTCCAGCACAGTACAAATGTACACATGGAAATTAGCCAGT 1420

QY 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATC 845
Db 1421 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGGTAGTAATTAGATC 1480

QY 846 TGAAAAATTTCCAGACAAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT 905
Db 1481 CGCCAAATTTCCGGGACAATGCTAAAGTCAATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540

QY 906 TAATTGTACAAGACCCCAACAATAACAAGAAAGGTTATCTATAGGACCCAGGAGAGC 965
Db 1541 TAATTGTACAAGACCCCAACAATAACAAGAAAGTATACATATAGGACCCAGGAGAGC 1600

QY 966 ATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACATTGTGAACATTAGTAG 1025
Db 1601 ATTTTATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTGAACCTTAGTAG 1660

QY 1026 AGCAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAAAATTAAAGAGAAAAATTTAGGAA 1085
Db 1661 AGCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAAAATTAAAGAGAACAAATTTGGGAA 1720

QY 1086 TAAACAATAGCCTTTAAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCAGATTT 1145
Db 1721 TAAACAATAGTCTTTAAGCACTCCTCAGGAGGGGACCCAGAAATTTGTACGCGCACAGTTT 1780

QY 1146 TAATTGTGGAGGGGAATTCCTTACTGTAATACAGCACAACTGTTTAAATAGTACTTGGAA 1205
Db 1781 TAATTGTGGAGGGGAATTTTCTACTGTAATTAACAACAACACTGTTTAAATAGTACTTGGAA 1840

QY 1206 TGTACTGGAGGGACAAATGCGCACTGAAGGAAATGACATAATCACACTCCAATGCGAGAA 1265
Db 1841 TGTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACAACATCACACTCCCATGCGAGAA 1900

QY 1266 AAAAAAAATTATAATATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCCCTCCCATCAC 1325
Db 1901 AAAAAAAATTATAAACATGTGGCAGGAAGTAGGAAAGCAATGTATGCCCCCTCCCATCAG 1960

QY 1326 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAA 1385
Db 1961 AGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG--- 2017

QY 1386 TAGTACTGAGACTGAGACTGAGATCTTTCAGACCTTGAGGAGGAGATATGAGGGACAATTG 1445
Db 2018 TCCTGAGGACAACAAGACCGAGGTCTTCAGACCTTGAGGAGGAGATATGAGGGATAATTG 2077

QY 1446 GAGAAAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCAC 1505
Db 2078 GAGAAAGTGAATTATATAATAATAAAGTAGTAATAAATTGAACCATTAGGAGTAGCACCCAC 2137

QY 1506 CAGGGCAAAGAGAGAAACAGTGCAAAAGAGAAAAAAGACCGG 1546
Db 2138 CAAGGCAAAGAGAGAGTGGTGCAGAGAGAAAAAAGAGCAG 2178

RESULT 4
US-08-417-210A-78/c
; Sequence 78, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-417-210A-78

Query Match 57.9%; Score 1174.2; DB 2; Length 3807;
Best Local Similarity 88.1%; Pred. No. 1.2e-291;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111
Db 1668 TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 1609

QY 112 AAATTGTGGGTCACAGTCTATTATATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTA 171
Db 1608 AAATTGTGGGTCACAGTCTATTATATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTA 1549

QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACAT 231
Db 1548 TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGGCCACACAT 1489

QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAAT 291
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGTAAATGTGACAGAAAAAT 1429

QY 292 TTAAACATGTGGAATAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
Db 1428 TTAAACATGTGGAATAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGG 1369

QY 352 GATGAAAGCCCTAAAGCCATGTGTAAATAATTAACCCCACTGTGTGTACTTTAAATTGCAC 411
Db 1368 GATCAAGCCCTAAAGCCATGTGTAAATAATTAACCCCACTGTGTGTACTTTAAATTGCAC 1309

QY 412 AATTG-----AATACACTAAGAAATACTACTAAATCCCACACTAGTAGCAGCTGG 459
Db 1308 GATTGAGGAATACTACTAATAACCAATAATAGTACTGCTAAATAACCAATAGTAATAGCGAG 1249

QY 460 GGAATGATGGAGAAAGGAGAAATAAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGA 519
Db 1248 GGAACAATAAAGGGAGGAGAAATGAAAAAAGCTGCTCTTTCAATATCACCACAAGCATAAGA 1189

QY 520 AATAAGGTAAGAAAGAATATGCACCTTTTAAATAGACTTTGATGTAGTACCATAAGAAAAAT 579
Db 1188 GATAAGATGCAGAAAGAATATGCACCTCTTTATAAACCTTGATATAGTATCAAT---AAAT 1132

QY 580 ACTAATAATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGT 639
Db 1131 AATGATAGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTGT 1072

QY 640 CCAAAGGTATCCTTTTCAGCCAAFTCCCATACATATTATTGTGTCCGGCTGGGTTTGGCATG 699
Db 1071 CCAAAGATATCCTTTTGAGCCAAFTCCCATACACTATTGTGTGCCCGGCTGGTTTGGCAT 1012

QY 700 CTAAAGTGTAACAATAAGACATTCAATGGATCAGGACCATGCACAAAATGTGAGCAGTA 759
Db 1011 CTAAAGTGTAACGATAAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAATGTGAGCAGTA 952

QY 760 CAATGTACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTA 819
Db 951 CAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTA 892

QY 820 GCAGAAAGAAGACATAGTAATTAGATCTGAAAAATTTTCAGACACAATGCTAAAAACCATAA 879
Db 891 GCAGAAAGAAGAGGTAGTAATTAGATCTGAGAATTTCAATGATAATGCTAAAAACCATCAT 832

QY 880 GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGA 939
Db 831 GTACATCTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAAGAAAA 772

QY 940 AGGTTATCTATAGGACCAGGGAGAGCATTTTATGCAAGAAGAAAAACATAATAGGAGATATA 999
Db 771 AGGATACATATAGGACCAGGGAGAGCATTTTATACAACAACAAAAATATATAGGAACATA 712

QY 1000 AGACAAAGCACATTTGAACATTAGTAGAGCAAAAATGGAATAAACACTTTTACAACAGATAGTT 1059
Db 711 AGACAAAGCACATTTGAACATTAGTAGAGCAAAAATGGAATGACACTTTAAGACAGATAGTT 652

QY 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAAAAACAATAGCCTTTTAATCAATCCTCAGGAGG 1119
Db 651 AGCAAAATTAAGAGAACAAATTTAAGAATAAAAAACAATAGTCTTTAATCAATCCTCAGGAGG 592

QY 1120 GACCCAGAAAATTGTAAATGCACAGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATACA 1179
Db 591 GACCCAGAAAATTGTAAATGCACAGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATCA 532

QY 1180 GCACAACTGTTTAAATAGTACTTTGGAATGTTTACTGGAGGGACAAAATGGCACTGAAG--A 1236
Db 531 TCACCACTGTTTAAATAGTACTTTGGAATGGTAATAATACTTGGAAATAATACTACAGGTCA 472

QY 1237 AATGACATAATCACACTCCCAATGCAGAATAAAAAACAATAATAAATATGTGGCAGAAAGTA 1296
Db 471 AATAACAATATCACACTTCAATGCAAAATAAAAAACAATAATAAACAATGTGGCAGGAAGTA 412

QY 1297 GGAAAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATATACA 1356
Db 411 GGAAAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATATACA 352

QY 1357 GGGCTGCTACTAACAAAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTC 1413
Db 351 GGGCTACTATTAACAAAGAGATGGTGTAGGACACCGACACGAAACGACACCGAGATCTTC 292

QY 1414 AGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTA 1473
Db 291 AGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAAGTGAATTATATAAATATAAAGTA 232

QY 1474 GTAAGAATTGAACCAATAGGAGTAGCACCCACCAGGGCAAAAGAGAAGAACAGTGCAAGA 1533
Db 231 GTAACAATTGAACCAATTAGGAGTAGCACCCACCAGGCAAAAGAGAAGAGTGGTGCAGAGA 172

QY 1534 GAAAAAAGA 1542
Db 171 GAAAAAAGA 163

RESULT 5
US-09-136-159A-78/c
; Sequence 78, Application US/09136159A
; Patent No. 6596279
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136,159A



; CURRENT FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: US 08/417,210  
; PRIOR FILING DATE: 1995-04-05  
; PRIOR APPLICATION NUMBER: US 08/223,842  
; PRIOR FILING DATE: 1994-04-06  
; PRIOR APPLICATION NUMBER: US 07/897,382  
; PRIOR FILING DATE: 1992-06-11  
; PRIOR APPLICATION NUMBER: US 07/715,921  
; PRIOR FILING DATE: 1991-06-14  
; PRIOR APPLICATION NUMBER: US 08/105,483  
; PRIOR FILING DATE: 1993-08-12  
; PRIOR APPLICATION NUMBER: US 07/847,951  
; PRIOR FILING DATE: 1992-03-06  
; PRIOR APPLICATION NUMBER: US 07/713,967  
; PRIOR FILING DATE: 1991-06-11  
; PRIOR APPLICATION NUMBER: US 07/666,056  
; PRIOR FILING DATE: 1991-03-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 3807  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand  
US-09-136-159A-78

	Query Match	57.9%;	Score 1174.2;	DB 4;	Length 3807;
	Best Local Similarity	88.1%;	Pred. No. 1.2e-291;		
	Matches 1330;	Conservative	0;	Mismatches 158;	Indels 21; Gaps 4;

  

QY	52	TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	1668	TGGGGTGGAGATGGGGCCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	1609
QY	112	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCCTCTA	171
Db	1608	AAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCCTCTA	1549
QY	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	1548	TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT	1489
QY	232	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTTGGGAAATGTGACAGAAAT	291
Db	1488	GCCTGTGTACCCACAGACCCCAACCCCAAGAAGTAGAATTGGTAAATGTGACAGAAAT	1429
QY	292	TTTAAACATGTGAAAAATAACATGCTAGATCAGATGCTAGGAGATATAATCAGTTTATGG	351
Db	1428	TTTAAACATGTGAAAAATAACATGCTAGAACAGATGCTAGGAGATATAATCAGTTTATGG	1369
QY	352	GATGAAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACT	411
Db	1368	GATCAAGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTAAATTGCACT	1309
QY	412	AATTG-----AATATCACTAAGAAATACTACTAATCCCACCTAGTAGCAGCTGG	459
Db	1308	GATTGAGGAATACTACTAATACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGAG	1249
QY	460	GGATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATATCACCACAAGCATAAGA	519
Db	1248	GGAAACAATAAAGGGAGAGAAATGAAAAAATGCTCTTTTCAATATCACCACAAGCATAAGA	1189
QY	520	AATAAGGTAAAGAAAGAAATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAT	579
Db	1188	GATAAGATGCAGAAAGAAATATGCACCTCTTTATAAACCTTGATATAGTATCAAT---AAAT	1132
QY	580	ACTAATAACTAAGTATAGTTTAAAGTTGTAACACCTCAGTCATTAACAGGSCCTGT	639
Db	1131	AATGATAGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTAACAAGCTTGT	1072
QY	640	CCAAAGGTATCCTTTTCAGCCAATTCCCATACATTATTGTGTCCCGGCTGGTTTGGCATG	699

Db	1071	CCAAAGATATCCTTTGAGCCAAATCCCATACACTATTGTGCCCCGGCTGGTTTTCGATT	1012
QY	700	CTAAAGTGTAACAATAAGACACTTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTA	759
Db	1011	CTAAAGTGTAACGATAAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAATGTCAGCACAGTA	952
QY	760	CAATGTACACATGGAAATAGGCCAGTGGTGTCAACTCAACTGCTGTAAAATGGCAGTCTTA	819
Db	951	CAATGTACACATGGAAATAGGCCAGTGGTGTCAACTCAACTCAACTGCTGTAAAATGGCAGTCTTA	892
QY	820	GCAGAAAGACACATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAAACCATATA	879
Db	891	GCAGAAAGAGAGGTAGTAATTAGATCTGAGAAATTTCAATGATAATGCTAAAAACCATATA	832
QY	880	GTACAGCTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGA	939
Db	831	GTACATCTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAAGAAA	772
QY	940	AGGTTATCTATAGGACCAGGGAGAGCATTTTATGCAAGAAAGAACATAATAGGAGATATA	999
Db	771	AGGATACATATAGGACCAGGGAGAGCATTTTATACAAACAAAAATATAATAGGAACTATA	712
QY	1000	AGACAAAGCACATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTT	1059
Db	711	AGACAAAGCACATTGTAACATTAGTAGAGCAAAATGGAATAACACTTTTAAAGACAGATAGTT	652
QY	1060	ATAAAATTAAAGAGAAAAATTTAGGAATAAAAAACAATAGCCTTTAATCAATCCTCAGGAGG	1119
Db	651	AGCAAATTAAAGAAACAATTTAAGAATAAAAAACAATAGTCTTTAATCAATCCTCAGGAGG	592
QY	1120	GACCCAGAAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAATACA	1179
Db	591	GACCCAGAAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTAATCA	532
QY	1180	GCACAACTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGACAAAATGGCACTGAAGG--A	1236
Db	531	TCACCACTGTTTAAATAGTACTTGGAAATGTTAAATACTTGGAAATAATACTACAGGTCA	472
QY	1237	AATGACATAATCACACTCCAATGCAGAATAAAAAACAATTAATAATATGTGGCAGAAAGTA	1296
Db	471	AATAACAATATCACACTTCAATGCAAAATGCAAAATTAACAATTAATAAACATGTGGCAGGAAGTA	412
QY	1297	GGAAAAAGCAATGTATGCCCTCCCCTCACAGGACAAATTAGATGTTTCATCAAAATATTACA	1356
Db	411	GGAAAAAGCAATATATGCCCTCCCCTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA	352
QY	1357	GGGCTGCTACTAAACAAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTC	1413
Db	351	GGGCTACTATTAAACAAGAGATGGTGTAAAGGACACGGACACGAACGACCCGAGATCTTC	292
QY	1414	AGACCTGGAGGAGAGATATAGGGGACAAATTTGGAGAGTGAATTATATAAATATAAAGTA	1473
Db	291	AGACCTGGAGGAGAGATATAGGGGACAAATTTGGAGAGTGAATTATATAAATATAAAGTA	232
QY	1474	GTAAGAATTGAACCAATAGGAGTAGCACCCACCGAGGCAAGAGAGAAACAGTGCAAGA	1533
Db	231	GTAACAATTGAACCAATTAGGAGTAGCACCCACCAAGGCAAGAGAGAGTGGTGCAGAGA	172
QY	1534	GAIAAIAAAGA 1542	
Db	171	GAIAAIAAAGA 163	

RESULT 6  
US-08-448-603A-27  
; Sequence 27, Application US/08448603A  
; Patent No. 5864027  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; APPLICANT: Nakamura, Gerald R.  
; TITLE OF INVENTION: HIV Envelope Polypeptides  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
STREET: 3 Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,603A  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/072,833  
FILING DATE: 07-JUN-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Haliday, Emily  
REGISTRATION NUMBER: 38903  
REFERENCE/DOCKET NUMBER: 14918-704  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2552 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2552  
US-08-448-603A-27

Query Match 57.8%; Score 1172.6; DB 2; Length 2552;  
Best Local Similarity 89.2%; Pred. No. 2.6e-291;  
Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

QY	64	TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGGGGTC	123
Db	46	TGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAGAAAAATTGGGGTC	105
QY	124	ACAGTCTATTATGGGGTACCTGTGTGGAGAGCAACACCACCTCTATTTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGGTACCTGTGTGGAAAGCAACACCACCTCTATTTTTGTGCATCA	165
QY	184	GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC	243
Db	166	GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC	225
QY	244	ACAGACCCCAACCCACAGAAGTAGTATTGGGAAATGTACAGAAAAATTTTAAACATGTGG	303
Db	226	ACAGACCCCAACCCACAGAAATAGGATTGGAAATGTAAACAGAAAAATTTTAAACATGTGG	285
QY	304	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAGCCCTA	363
Db	286	AAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAGCTTA	345
QY	364	AAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTCACACTAAATTTGAATATC	423
Db	346	AAGCCATGTGTAAAAATTAAACCCCACTATGTGTTACTTTAAATTCACACTGATTG-----	399
QY	424	ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA	483
Db	400	---AAAAATGCTACTAATACCACTAGTAGCAGCTGGGGAAGATGGAGAGAGGAGAAATA	456
QY	484	AAAAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCA	543
Db	457	AAAAACTGCTCTTTCAATGTCAACCAAGTATAAGAGATAAGATGAAGATGAATATGCA	516

QY	544	CTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAATAATACTAAGTATAGGTTA	603
Db	517	CTTTTATAAACTTGATGTAGTACCAATAG---ATAATGATAATACTAGCTATAGGTTG	573
QY	604	ATAAGTTGTAAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCCTTTCAGCCAATT	663
Db	574	ATAAGTTGTAAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTGTCTCTTGAGCCAATT	633
QY	664	CCCATACATTATTGTGTCCTGGGCTGGGTTTCGGATGCTAAAGTGTAAACAATAAGACATTC	723
Db	634	CCCATACATTATTGTGTCCTGGGCTGGTTCGGATGCTAAAGTGTAGAGATAAAAAGTTTC	693
QY	724	AATGGATCAGGACCATGCACAAAATGTTCAGCACAGTACAAATGTACACATGGAATTAGCCCA	783
Db	694	AACGGAACAGGACCATGTACAAATGTTCAGCACAGTACAAATGTACACATGGAATTAGCCCA	753
QY	784	GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA	843
Db	754	GTAGTATCAACTCAACTGCTGTTAAATGGCAGTTTAGCAGAAAGAAAGTAGTAATTAGA	813
QY	844	TCTGAAAAATTTACAGACAATGCTAAAAACCATATAATAGTACAGCTAAATGAAATCTGTAGTA	903
Db	814	TCTGCCAATTTCTCGACAATGCTAAAAACCATATAATAGTACAGCTGAACGAATCTGTAGAA	873
QY	904	ATTAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGA	963
Db	874	ATTAATTGTACAAGACCCCAACAACAATACAAGAAAGTATACATATAGGACCAGGGAGA	933
QY	964	GCATTTTATGCAAGAAACAATAATAGGAGATATAAGACAAGCACATTGTGAACCTTAGT	1023
Db	934	GCATTTTATGCAACAGGAGAAATAATAGGAGACATAAGACAAGCACATTGTGAACCTTAGT	993
QY	1024	AGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGG	1083
Db	994	AGCACAAAAATGGAATAATACTTTTAAACACAGATAGTTACAAAAATTAAGAGAACATTTT---	1050
QY	1084	AATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAATTTGTAATGCACAGT	1143
Db	1051	AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGACCCAGAAAATTTGTAATGCACAGT	1110
QY	1144	TTTAATTGTGGAGGGGAATTTCTTACTGTATAATACAGCACAACTGTTTAAATAGTACTTGG	1203
Db	1111	TTTAATTGTGGAGGGGAATTTTCTACTGTATAACAACACCACTGTTTAAATAGTACTTGG	1170
QY	1204	AATGTTACTGGAGGGACAAATGGCACCTGAAGGAAATGA-----CATAAATCACA	1251
Db	1171	AATTATACCTTATCTTGAATAATACTGAAGGGTCAAAATGACACTGGAAGAAATATCACA	1230
QY	1252	CTCCAATGCAGATAAAACAATAATAATAATGTGGCAGAAAAGTAGGAAAAGCAATGTAT	1311
Db	1231	CTCCAATGCAGATAAAACAATAATAATAATGTGGCAGGAAAGTAGGAAAAGCAATGTAT	1290
QY	1312	GCCCTCCCATCAGGACAAAATTAGATGTTTCATAATAATATTACAGGGCTGCTACTAACA	1371
Db	1291	GCCCTCCCATAGAGGACAAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTAAACA	1350
QY	1372	AGAGATGGAGGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT	1431
Db	1351	AGAGATGGTGGTAATA-----ACAGCGAAACCAGATCTTCAGACCTGGAGGAGAGAT	1404
QY	1432	ATGAGGGACAATTGGAGAAAGTGAATTATATAATAATAAGTAGTAAGAATTTGAACCAATA	1491
Db	1405	ATGAGGGACAATTGGAGAAAGTGAATTATATAATAATAAGTAGTAAGAAATTTGACCATT	1464
QY	1492	GGAGTAGCACCCACAGGGCAAGAGAAAGACAGTGCAGAAAGAAAAAGACCCG	1546
Db	1465	GGAGTAGCACCCACAGGGCAAGAGAAAGAGTGTATGCAGAGAGAAAAAGAGCAG	1519

RESULT 7  
US-09-134-075-27  
; Sequence 27, Application US/09134075

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; Patent No. 6042836
;
; GENERAL INFORMATION:
;
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
;
; NUMBER OF SEQUENCES: 33
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
;
; OPERATING SYSTEM: DOS
;
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/134,075
;
; FILING DATE:
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 08/448,603
;
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Haliday, Emily
;
; REGISTRATION NUMBER: 38903
;
; REFERENCE/DOCKET NUMBER: 14918-704
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 415-393-2000
;
; TELEFAX: 415-393-2286
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 27:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2552 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: 1..2552
;
; US-09-134-075-27

```

```
Query Match          57.8%; Score 1172.6; DB 3; Length 2552;
Best Local Similarity 89.2%; Pred. NO. 2.6e-291;
Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;
```

64	QY	TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC	123
46	Db	TGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAGAAAAATTGTGGGTC	105
124	QY	ACAGTCTATTATGGGTACCTGTGTGGAGAGAAGCAACCAACCACTCTATTTTGTGCAATCA	183
106	Db	ACAGTCTATTATGGGTACCTGTGTGGAAGAAGCAACCAACCACTCTATTTTGTGCAATCA	165
184	QY	GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC	243
166	Db	GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC	225
244	QY	ACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG	303
226	Db	ACAGACCCCAACCCACAAGAATAAGGATTGGAAAAATGTAAACAGAAAAATTTTAAACATGTGG	285
304	QY	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
286	Db	AAAAATAACATGGTAGAAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAAGCTTA	345
364	QY	AAGCCATGTGTAAATAAATTAACCCCACTCTGTGTTACTTTTAAATTTGCACTAATTTGAATATC	423
346	Db	AAGCCATGTGTAAATAAATTAACCCCACTATGTGTACTTTAAATTTGCACTGATTTG-----	399



Db 1465 GGAGTAGCACCACCAAGGCAAGAGAGAGAGTGATGCAGAGAGAGAGAGAGCAG 1519

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RESULT 8

US-09-492-739-27

; Sequence 27, Application US/09492739

; Patent No. 6331404

; GENERAL INFORMATION:

; APPLICANT: Berman, Phillip W.

; Nakamura, Gerald R.

; TITLE OF INVENTION: HIV Envelope Polypeptides

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP

; STREET: 3 Embarcadero Center

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/492,739

; FILING DATE: 27-Jan-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/134,075

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Haliday, Emily

; REGISTRATION NUMBER: 38903

; REFERENCE/DOCKET NUMBER: 14918-704

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-393-2000

; TELEFAX: 415-393-2286

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 2552 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2552

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-492-739-27

Query Match 57.8%; Score 1172.6; DB 3; Length 2552;

Best Local Similarity 89.2%; Pred. No. 2.6e-291;

Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

Qy 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC 123

Db 46 TGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAGAAAAATTGTGGGTC 105

Qy 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTTTGTGCATCA 183

Db 106 ACAGTCTATTATGGGGTACCTGTGTGGAAGAAGCAACCACTCTATTTTGTGCATCA 165

Qy 184 GATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 243

Db 166 GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 225

Qy 244 ACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACATGTGG 303

Db 226 ACAGACCCCAACCCACAAGAAATAGGATTGGAAAATGTTAACAGAAAAATTTTAACATGTGG 285

Qy 304 AAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363

Db 286 AAAAAATAACATGGTAGAACACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCTTA 345

Qy 364 AAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTGCACATAATTGGAATATC 423

Db 346 AAGCCATGTGTAAAAATTAAACCCCACTATGTGTTACTTTTAAATTGCACATGATTG----- 399

Qy 424 ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA 483

Db 400 ---AAAAATGCTACTAATAACCACTAGTAGCAGCTGGGGAAGATGGAGAGAGGAGAAATA 456

Qy 484 AAAAAATTGCTCTTTCTATATCACCACAAGCATATAAGAAATAAGGTAAAGAAAGAAATATGCA 543

Db 457 AAAAACTGCTCTTTCAATGTCCACCACAAGTATAAGAGATAAGATGAAGAATGAATATATGCA 516

Qy 544 CTTTTTAATAGACTTGTATGTAGTACCATAATAGAAAAATACTAATAATACTAAGTATAGGTTA 603

Db 517 CTTTTTTATAAACTTGATGTAGTACCAATAG--ATAATGATAATACTAGCTATAGGTTG 573

Qy 604 ATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAAGGTATCCTTTCAGCCCAATT 663

Db 574 ATAAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAAGGTGTCTTTGAGCCCAATT 633

Qy 664 CCCATACATTATTGTGTCCGGCTGGGTTTGGCATGCTTAAAGTGTAAACAATAAGACATTTC 723

Db 634 CCCATACATTATTGTGCCCGCGCTGGTTTTCGGATTCTTAAAGTGTAGAGATAAAAAAGTTTC 693

Qy 724 AATGGATCAGGACCATGCAAAAATGTACACACAGTCAGCACAGTACAAATGTACACATGGAATTAGGCCA 783

Db 694 AACGGAACAGGACCATGTACAAAATGTACAGCACAGTACAAATGTACACATGGAATTAGGCCA 753

Qy 784 GTGGTGTCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGA 843

Db 754 GTAGTATCAACTCAACTGCTGTAAATGGCAGTTTAGCAGAAGAAGTAGTAATTAGA 813

Qy 844 TCTGAAAAATTTACAGACAAATGCTAAACCATAATAGTACAGCTAAATGAATCTGTAGTA 903

Db 814 TCTGCCAATTTCTCGGACAAATGCTAAACCATAATAGTACAGCTGAACGAATCTGTAGAA 873

Qy 904 ATTAATTGTACAAGACCCCAACAACAATACAAGAAGAGGTTATCTATAGGACCAGGGAGA 963

Db 874 ATTAATTGTACAAGACCCCAACAACAATACAAGAAGAGTATACATATAGGACCAGGGAGA 933

Qy 964 GCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGT 1023

Db 934 GCATTTTATGCAACAGGAGAAAAATAATAGGAGACATAAGACAAGCACATTGTACCTTAGT 993

Qy 1024 AGAGCAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAAATTAAAGAGAAAAATTTAGG 1083

Db 994 AGCACAAAATGGAATAATACTTTTAAACAGATAGTTTACAAAATTAAAGAGAACATTTT--- 1050

Qy 1084 AATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCAGAAAATTGTAATGCACAGT 1143

Db 1051 AATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCCAGAAAATTGTAATGCACAGT 1110

Qy 1144 TTTAATTGTGGAGGGGAATTCTTCTACTGTAATACAGCACAACTGTTTTAATAGTACTTTGG 1203

Db 1111 TTTAATTGTGGAGGGGAATTTTCTACTGTAATACAAACCACTGTTTAAATAGTACTTTGG 1170

Qy 1204 AATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGA-----CATAATCACA 1251

Db 1171 AATTATACTTATACTTTGGAATAATACTCTGAAGGGTCAATGACACTGGAAGAAATATCACA 1230

Qy 1252 CTCCAATGCAGAATAAAAACAATAATATAAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1311

Db 1231 CTCCAATGCAGAATAAAAACAATAATATAAACAATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1290

Qy 1312 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATAATTACAGGGCTGCTACTAACA 1371

Db 1291 GCCCTCCCATTAAGAGGACAAATTAGATGCTCATCAATAATTACAGGGCTGCTATTAAACA 1350

Qy 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTCGAGGAGGAGAT 1431



QY	1363	CTACTAAC	AAGAGATGGAGGTAATAGTACTGA	---	GACTGAGAC	TGAGATCTTCAGACCT	1419
Db	1357	CTATTAA	CAAGAGATGGTGGTAAGGACACGGACACGAA	CGACCCGAGATCTTCAGACCT			1416
QY	1420	GGAGGAGGAGATATGAGGGACAAT	TGGAGAAGTGAATTATATAAATATAAA	GTAGTAAGA			1479
Db	1417	GGAGGAGGAGATATGAGGGACAAT	TGGAGAAGTGAATTATATAAATATAAA	GTAGTAACA			1476
QY	1480	ATTGAACCAATAGGAGTAGCACC	CCAGGGCAAAGAGAAGAAACAGTGC	AAAGAGAAAAA			1539
Db	1477	ATTGAACCAATTAGGAGTAGCACC	CAAGGCAAGAGAAGAGTGGTGC	AGAGAGAAAAA			1536
QY	1540	AGACCGGATCCAGAA		1554			
Db	1537	AGAGCAGCGATAGGA		1551			

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RESULT 10
US-08-475-391-3
; Sequence 3, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786211and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-475-391-3

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QY	178	GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGT	237
Db	160	GCATCAGATGCTAAAGCATAATGATACAGAGGTACATAAATGTTTGGGCCACACAGCCTGT	219
QY	238	GTACCCACAGACCCCAACCCACAAAGAGTAGTATGGGAAATGTGACAGAAAATTTTAAC	297
Db	220	GTACCCACAGACCCCAACCCACAAAGAGTAGAATGGTAAATGTGACAGAAAATTTTAAC	279
QY	298	ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA	357
Db	280	ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA	339
QY	358	AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTTGCACTAATTTG	417
Db	340	AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTTGCACTGATTTG	399
QY	418	-----AATATCACTAAGAAATACCTAAATCCCACCTAGTAGCAGCTGGGGAATG	465
Db	400	AGGAATACTACTAATAACCAATAATAGTACTGCTAAATAACAATAGTAATAGCGAGGGAACA	459
QY	466	ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAAAATAAG	525
Db	460	ATAAAGGGAGGAGAAATGAAAACTGCTCTTTCAATATCACCACAAGCATAAGAGATAAG	519
QY	526	GTAAGAAAAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT	585
Db	520	ATGCAGAAAGAAATATGCACCTTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT	576
QY	586	AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAG	645
Db	577	AGTACCAGCTATAGGTTGATAAGTTGATAAAGTTGATAAAGCTCAGTCATTACACAAGCTTGTCCAAAG	636
QY	646	GTATCCTTTCAGCCAAATCCCATACATTATTGTGTCCCGGCTGGTTTTCGATGCTAAAG	705
Db	637	ATATCCTTTGAGCCAAATCCCATACACTATTGTGCCCCGGCTGGTTTTCGATTTCTAAAA	696
QY	706	TGTAACAATAAGACATTTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGT	765
Db	697	TGTAACGATAAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAATGTGAGCACAGTACAATGT	756
QY	766	ACACATGGAAATTAGGCCAGTGGTGTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAA	825
Db	757	ACACATGGAAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	816
QY	826	GAAGACATAGTAATTAGATCTGAAAAATTTCAAGACAAATGCTAAAAACCAATAATAGTACAG	885
Db	817	GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGATAATGCTAAAAACCATCATAGTACAT	876
QY	886	CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAGAAGAAGGTTA	945
Db	877	CTGAATGAATCTGTACAAATTAATTGTACAAGACCCCAACTACAATAAAGAAAAAGGATA	936
QY	946	TCTATAGGACACGGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA	1005
Db	937	CATATAGGACACGGGAGAGCATTTTATACAAACAAAAATATAATAGGAACCTATAAGACAA	996
QY	1006	GCACATTGTAACATTAGTAGAGCAAAAATGGAATAAACACTTTTACAACAGATAGTTATAAAA	1065
Db	997	GCACATTGTAACATTAGTAGAGCAAAAATGGAATGACACTTTTAAGACAGATAGTTAGCAAA	1056
QY	1066	TTAAGAGAAAAATTTAGGAATAAAAAATAAGCCTTTTAATCAATCCTCAGGAGGGACCCA	1125
Db	1057	TTAAAGAACAAATTTAAGAAATAAAACAATACTCTTTAATCAATCCTCAGGAGGGACCCA	1116
QY	1126	GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTCTTCTACTGTATAACAGCACAA	1185
Db	1117	GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTTCTACTGTATAACATCACCA	1176
QY	1186	CTGTTTAAATAGTACTTGAATG--TTACTGGAGGGACAAAATGGCACTGAAGGAATGAC	1242
Db	1177	CTGTTTAAATAGTACTTGAATGGTAATAATACTTTGGAATAATACTACAGGTCAAAATAAC	1236





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QY 1186 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242
D 1177 CTGTTTAAATAGTACTTTGGAATGGTAAATAATACTTTGGAATAATACTACAGGGTCAAATAAC 1236
QY 1243 ATAATCACACTCCAATGCAGAAATAAAACAAATTAATAATATGTGGCAGAAAAGTAGGAAAA 1302
D 1237 AATATCACACTTCAATGCAGAAATAAAACAAATTAATAACATGTGGCAGGAAAGTAGGAAAA 1296
QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362
D 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356
QY 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419
D 1357 CTATTAAACAAGAGATGGTGAAGGACACCGGACACGACACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTATATAATAATAAGTAGTAAGA 1479
D 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTATATAATAATAAGTAGTAACA 1476
QY 1480 ATTGAACCAATAGGATAGGACCCACAGGGCAAAGAGAAACAGTGCAAAGAGAAAAA 1539
D 1477 ATTGAACCAATAGGATAGGACCCACCAAGGCAAAGAGAAAGTGGTGCAGAGAGAAAAA 1536
QY 1540 AGACCGGATCCAGAA 1554
D 1537 AGACGAGCGATAGGA 1551
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RESULT 12

US-09-552-950-3

; Sequence 3, Application US/09552950

; Patent No. 6541248

; GENERAL INFORMATION:

; APPLICANT: Oxford Biomedica (UK) Limited

; TITLE OF INVENTION: Anti-Viral Vectors

; FILE REFERENCE: 674524-2004

; CURRENT APPLICATION NUMBER: US/09/552,950

; CURRENT FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2571

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-09-552-950-3

Query Match 57.8%; Score 1172.2; DB 4; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 3.2e-291;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

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QY 58 TCGGCTTCGAGATCCATGCTCCTTTGGGATATTGTATGATCTGTAGTGCTACAGAAAAATTG 117
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QY 118 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTTTGT 177
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D 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAAAGCCTGT 219
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D 220 GTACCCACAGACCCCAACCCACAAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAAC 279
QY 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357
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QY 358 AGCCTAAAGCCCATGTGTAAATAATAACCCCACTCTGTGTACTTTAAATTGCACTAATTG 417
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QY 1540 AGACCGGATCCAGAA 1554  
Db 1537 AGAGCAGCGATAGGA 1551

RESULT 13

US-09-936-572-3  
; Sequence 3, Application US/09936572  
; Patent No. 6783981  
; GENERAL INFORMATION:  
; APPLICANT: UDEN, MARK  
; APPLICANT: MITROPHANOUS, KYRIACOS  
; TITLE OF INVENTION: ANTI-VIRAL VECTORS  
; FILE REFERENCE: 078883/0137  
; CURRENT APPLICATION NUMBER: US/09/936,572  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: PCT/GB00/01002  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: GB 9906177.2  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2571  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-936-572-3

Query Match 57.8%; Score 1172.2; DB 4; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 3.2e-291;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
QY 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117  
Db 40 TGGGGATGGGCGACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGTCTACAGAAAAATTG 99  
QY 118 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACACCACCTCTATTTTGT 177  
Db 100 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACACCACCTCTATTTTGT 159  
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Db 280 ATGTGGAAAAATAACATGGTATGACACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339  
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QY 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
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QY 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATACCAACAGCATATAAGAAATAAG 525  
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Db 1477 ATTGAACCATTAGGAGTAGCACCCACCACCAAGGCAAGAGAGAGTGGTGCAGAGAGAAAA 1536  
QY 1540 AGACCGGATCCAGAA 1554  
Db 1537 AGAGCAGCGATAGGA 1551

RESULT 14  
PCT-US95-07178-3  
; Sequence 3, Application PC/TUS9507178



;  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07178  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US95-07178-3

Query Match 57.8%; Score 1172.2; DB 5; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 3.2e-291;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
  
QY 58 TCGGCTTCGAGATCCATGCTCCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117  
Db 40 TGGGGATGGGCGACGATGCTCCTGGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99  
  
QY 118 TGSGTCACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACCTCTATTTGT 177  
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Db 2380 AGAGCAGCGATAGGA 2366

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OM nucleic - nucleic search, using sw model

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Perfect score: 2028  
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Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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21:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1221.8	60.2	9540	17	US-10-325-468-46	Sequence 46, Appl
2	1198.8	59.1	2612	15	US-10-414-692-20	Sequence 20, Appl
3	1197	59.0	1512	9	US-09-759-841-3	Sequence 3, Appli
4	1179.8	58.2	1422	18	US-10-728-195-7	Sequence 7, Appli
5	1174.2	57.9	3807	15	US-10-441-788-78	Sequence 78, Appl
6	1172.6	57.8	2552	10	US-09-966-931-27	Sequence 27, Appl
7	1172.6	57.8	2552	17	US-10-459-121-27	Sequence 27, Appl
8	1172.2	57.8	2571	9	US-09-999-183-3	Sequence 3, Appli
9	1172.2	57.8	2571	13	US-10-077-294-3	Sequence 3, Appli
10	1172.2	57.8	2571	13	US-10-163-886-3	Sequence 3, Appli
11	1172.2	57.8	2571	14	US-10-263-127-3	Sequence 3, Appli
12	1172.2	57.8	2571	15	US-10-375-777-3	Sequence 3, Appli

13	1172.2	57.8	2571	16	US-10-351-938-3	Sequence 3, Appli
14	1169.4	57.7	2573	10	US-09-966-931-29	Sequence 29, Appl
15	1169.4	57.7	2573	17	US-10-459-121-29	Sequence 29, Appl
16	1166.4	57.5	9706	17	US-10-325-468-45	Sequence 45, Appl
17	1166.2	57.5	9704	17	US-10-325-468-40	Sequence 40, Appl
18	1164.6	57.4	9715	17	US-10-325-468-44	Sequence 44, Appl
19	1164.6	57.4	9942	17	US-10-325-468-5	Sequence 5, Appli
20	1164.6	57.4	9942	17	US-10-325-468-54	Sequence 54, Appl
21	1164.2	57.4	2627	15	US-10-177-390-9	Sequence 9, Appli
22	1163	57.3	9942	17	US-10-325-468-1	Sequence 1, Appli
23	1163	57.3	9942	17	US-10-325-468-2	Sequence 2, Appli
24	1163	57.3	9942	17	US-10-325-468-7	Sequence 7, Appli
25	1163	57.3	9942	17	US-10-325-468-50	Sequence 50, Appl
26	1163	57.3	9942	17	US-10-325-468-51	Sequence 51, Appl
27	1163	57.3	9942	17	US-10-325-468-56	Sequence 56, Appl
28	1161.8	57.3	1932	15	US-10-387-336-31	Sequence 31, Appl
29	1161.8	57.3	2457	15	US-10-387-336-32	Sequence 32, Appl
30	1161.4	57.3	9942	17	US-10-325-468-3	Sequence 3, Appli
31	1161.4	57.3	9942	17	US-10-325-468-52	Sequence 52, Appl
32	1161.2	57.3	2570	10	US-09-966-931-31	Sequence 31, Appl
33	1161.2	57.3	2570	17	US-10-459-121-31	Sequence 31, Appl
34	1161	57.2	1419	15	US-10-387-336-30	Sequence 30, Appl
35	1160.8	57.2	9737	10	US-09-827-688-12	Sequence 12, Appl
36	1160	57.2	1530	15	US-10-361-849-13	Sequence 13, Appl
37	1160	57.2	1929	14	US-10-032-162-12	Sequence 12, Appl
38	1159.8	57.2	9942	17	US-10-325-468-6	Sequence 6, Appli
39	1159.8	57.2	9942	17	US-10-325-468-55	Sequence 55, Appl
40	1148.6	56.6	2214	15	US-10-336-566-85	Sequence 85, Appl
41	1148.6	56.6	9505	15	US-10-336-566-9	Sequence 9, Appli
42	1148.6	56.6	9506	15	US-10-336-566-8	Sequence 8, Appli
43	1148.6	56.6	9544	9	US-09-798-675-4	Sequence 4, Appli
44	1148.6	56.6	9544	15	US-10-336-566-7	Sequence 7, Appli
45	1148.6	56.6	9545	17	US-10-093-953A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-325-468-46  
; Sequence 46, Application US/10325468  
; Publication No. US20040101823A1  
; GENERAL INFORMATION:  
; APPLICANT: Soong, Nay Wei  
; APPLICANT: Pekrun, Katja  
; APPLICANT: Shibata, Riri  
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL  
; FILE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS  
; FILE REFERENCE: 0166.210US  
; CURRENT APPLICATION NUMBER: US/10/325,468  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/343,524  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 9540  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus 1  
; FEATURE:  
; OTHER INFORMATION: parent JRCSEF DNA (GenBank Accession No. M38429)  
US-10-325-468-46

Query Match 60.2%; Score 1221.8; DB 17; Length 9540;  
Best Local Similarity 90.4%; Pred. No. 3.8e-273;  
Matches 1333; Conservative 0; Mismatches 127; Indels 15; Gaps 2;

QY	72	CATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGGTCCACAGTCTA	131
Db	6289	CTTGCTCCTTGGGACATTAAATGATCTGTAGTGTAGAAAAAGTTGTGGTCCACAGTCTA	6348
QY	132	TTATGGGGTACCTGTGTGGAGAGAAGCAACCACCACCTCTATTTTGTGCATCAGATGCTAA	191

Db 6349 TTATGGGTACCTGTGTGGAAGAAACAACCACTCTATTTTGTGTCATCAGATGCTAA 6408

QY 192 AGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 251

Db 6409 AGCATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCC 6468

QY 252 CAACCCACAAGAAGTAGTATTTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAA 311

Db 6469 CAACCCACAAGAAGTAGTATTTGGGAAATGTAAACAGAGATTTTAAACATGTGGAAAAATAA 6528

QY 312 CATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAAGCCTTAAAGCCATG 371

Db 6529 CATGGTAGAACAGATGCAGGAGGATGTAATCAATTTATGGGATCAAAGCTTAAAGCCATG 6588

QY 372 TGTAAAAATTAAACCCACTCTGTGTTACTTTTAAATTCGACTAATTTGAATATCACTAAGAA 431

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QY 432 TACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAAGGAGAAAATAAAAAATTG 491

Db 6637 TGCTACTAATACCACTAGTAGTAGTGAGGGAATGATGGAGAGGAGAGAAAATAAAAAAATG 6696

QY 492 CTCCTTTCTATATCACCACAAGCATAAAGAAATAAGGTAAGAAAAGAAATATGCACCTTTTAA 551

Db 6697 CTCCTTTCAATATCACCAAAAAGCATAAAGAGATAAGGTGCAGAAAAGATATGCTCTTTTAA 6756

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Db 6757 TAAACTGGATGTAGTACCAATAGATAATAAGAAATAATACCAAAATATAGTTTAAGTTG 6816

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Db 6817 TAAACCTCAGTCATTACACAAGCCTGTCCAAAGGTATCCTTTTGAACCAATTCCTATACA 6876

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Db 7057 TTTTACGGACAATGCTAAAACCATAAATAGTACAGCTGAATGAATCTGTAAAAATTAATTG 7116

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QY 1152 TGGAGGGGAATTTCTTACTGTGTAATACAGCACAACTGTTTAAATAGTACTTTGGAATGTTAC 1211

Db 7357 TGGAGGGGAATTTTCTACTGTGTAATTCACACAACTGTTTAAATAGTACTTTGGAATGATAC 7416

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Db 7417 TGAAGAGTCAAGTGGCACTGAAGGAAATGACACCATCATACTCTCCATGCAGAAATAAAAAACA 7476

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Db 7477 AATTATAAACATGTGGCAGGAAGTGGGAAAAGCAATGTATGCTCCTCCCATTAAGGACA 7536

QY 1332 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAAGAGATGGAGGTAATAGTAC 1391

Db 7537 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGTAA---AAA 7593

QY 1392 TGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGACAAATTGGAGAAAG 1451

Db 7594 TGAGAGTGAGATCGAGATCTTCAGACCTGGAGGAGAGACATGAGGGACAAATTGGAGAAAG 7653

QY 1452 TGAATTATATAATAATAAAGTAGTAAGAAATTGAAACCAATAGGAGTAGCACCCACAGGGC 1511

Db 7654 TGAATTATATAATAATAAAGTAGTAATAAATTGAAACCATTAGGAGTAGCACCCCAAGGC 7713

QY 1512 AAAGAGAAAGAACAGTGCAAAAGAGAAAAAAGACCGG 1546

Db 7714 AAAGAGAAAGATGGTGCAAAAGAGAAAAAAGAGCAG 7748

RESULT 2

US-10-414-692-20

; Sequence 20, Application US/10414692

; Publication No. US20030228607A1

; GENERAL INFORMATION:

; APPLICANT: X-Ceptor Therapeutics, Inc.

; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic

; TITLE OF INVENTION: profile

; FILE REFERENCE: 8012-002-US

; CURRENT APPLICATION NUMBER: US/10/414,692

; CURRENT FILING DATE: 2003-04-14

; PRIOR APPLICATION NUMBER: 60/372,650

; PRIOR FILING DATE: 2002-04-15

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20

; LENGTH: 2612

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-10-414-692-20

Query Match 59.1%; Score 1198.8; DB 15; Length 2612;

Best Local Similarity 90.5%; Pred. No. 4.8e-268;

Matches 1343; Conservative 0; Mismatches 117; Indels 24; Gaps 5;

QY 66 GAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAAATTGTGGGTCA 125

Db 442 GGGCACCTTGCTCCTTGGGATATTAATGATCTGTAGTCTGTAGAAAAAGTTGTGGGTCA 501

QY 126 AGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCAACCACCTCTATTTTGTGCATCAG 185

Db 502 AGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCAACCACCTCTATTTTGTGCATCAG 561

QY 186 TGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCAC 245

Db 562 TGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCAC 621

QY 246 AGACCCCAACCCACAAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAA 305

Db 622 AGACCCCAACCCCAAGAAAGTAGTATTGGAAAAATGTAAACAGAACATTTTAAACATGTGGAA 681

QY 306 AAATAAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCTAAA 365

Db 682 AAATAAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAA 741

QY 366 GCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCGACTAATTTGAATATCAC 425

Db 742 GCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTCGAAGGATGT----- 792

QY 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAA 485



Db 793 ---GAATGCTACTAATACCACTAATGATAGCGAGGGAACGATGGAGAGAGGAGAAATAAA 849

Qy 486 AAATTGCTCTTTCTATATACCACAAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACT 545

Db 850 AAATGCTCTTTCAATATACCACAAGCATAAAGAGATAGGTGCAGAAAGAAATATGCTCT 909

Qy 546 TTTTAATAGACTTGATGTAGTACCAATAGAAAATACTAATAATACTAAGATATAGGTTAAT 605

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Db 1207 TGACAATTTTACGGAACAATGCTAAAAACCATATAGTACAGCTGAAAGAAATCTGTAGAAAT 1266

Qy 906 TAATTGTACAAGACCCCAACAACAATAACAAGAAAGGTTATCTATAGGACCCAGGAGAGC 965

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Qy 966 ATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTAG 1025

Db 1327 ATTTTATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTAG 1386

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Qy 1263 AATAAAACAAATTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCAT 1322

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Qy 1323 CACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACAAGAGATGGAGG 1382

Db 1684 CAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG 1743

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Qy 1443 TTGAGAAGTGAATTATATAAATATAAAGTAGTAAGAAATGAACCAATAGGAGTAGCACC 1502

Db 1801 TTGAGAAGTGAATTATATAAATATAAAGTAGTAAGAAATGAACCATTAGGAGTAGCACC 1860

Qy 1503 CACCAGGGCAAAGAGAAAGACAGTGCAAAGAGAAAAAGACCGG 1546

Db 1861 CACCAAGGCAAAGAGAGAGTGGTGCAAGAGAAAAAGAGCAG 1904

RESULT 3

US-09-759-841-3  
; Sequence 3, Application US/09759841  
; Patent No. US20010039026A1  
; GENERAL INFORMATION:  
; APPLICANT: Rickett, Graham A  
; APPLICANT: Dobbs, Susan  
; APPLICANT: Perros, Manoussos  
; TITLE OF INVENTION: Assay Method  
; FILE REFERENCE: PC10348APME  
; CURRENT APPLICATION NUMBER: US/09/759,841  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1512  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-759-841-3

Query Match 59.0%; Score 1197; DB 9; Length 1512;  
Best Local Similarity 89.2%; Pred. No. 9.8e-268;  
Matches 1316; Conservative 0; Mismatches 150; Indels 9; Gaps 2;

Qy 74 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTGTGGTCCACAGTCTATT 133

Db 38 TGCTGTGTGGAGCAGTCTTCGTTTCGGCTAGCGTAGAAAAAATTGTGGTCCACAGTTTATT 97

Qy 134 ATGGGGTACCTGTGTGGAGAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATGCTAAAG 193

Db 98 ATGGGGTACCTGTGTGGAAAGAAAGCAACCACCACCTCTATTTTGTGCATCAGATGCTAAAG 157

Qy 194 CCTATGATACAGAGGTACATAATGTTTGGGGCCACACATGCCTGTGTACCCACAGACCCCA 253

Db 158 CATATGATACAGAGGTACATAATGTTTGGGGCCACACATGCCTGTGTACCCACAGACCCCA 217

Qy 254 ACCACAAGAAAGTAGTATTGGGAAATGTGACAGAAATTTTAAACATGTGGAAAAATAACA 313

Db 218 ACCACAAGAAAGTAGAATTGGAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 277

Qy 314 TGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCCATGTG 373

Db 278 TGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTG 337

Qy 374 TAAAAATTAACCCCACTGTGTGTACTTTAAATTCACATAATTGA-----ATATCACTA 427

Db 338 TAAAAATTAACCTCACTGTGTGTACTTTAAATTCACATGATTTGAGGAATGCTACTAATG 397

Qy 428 AGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAAA 487

Db 398 GGAATGACACTAATACCACCTAGTAGTAGCAGGGGAAATGATGGGGGAGGAGAAATGAAA 457

Qy 488 ATTGCTCTTTCTATATCAACCAAGCATAGAATAAGGTAAAGAAAGAAATATGCACTTT 547

Db 458 ATTGCTCTTTCAAAATCACCAAAACATAAGAGGTAAAGGTGAGAAAGAAATATGCACTTT 517

Qy 548 TTAATAGACTTGATGTFAGTACCAATAGAAAAATACTTAATACTAAGTATAGGTTAATAA 607

Db 518 TTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAATAATAGATATAGGTTGATAA 577

Qy 608 GTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTTCAGCCCAATCCCA 667

Db 578 GTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCCAATCCCA 637

Qy 668 TACATTATTGTGTCCCGCTGGGTTTTCGGATGCTTAAAGTGTAAACAATAAGACATTCAATG 727

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Db 638 TACATTATTGTCCTCCCGCTGGTTTTGGGATCTCTAAAGTGTAAAGATAAGAAGTTCAATG 697
QY 728 GATCAGGACCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGG 787
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QY 788 TGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAACACATAGTAATTTAGATCTG 847
Db 758 TATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAAGAGGTAGTAATTAGATCCG 817
QY 848 AAAATTTACAGACAATGCTAAAAACCATAATAGTACAGCTAAATGAATCTGTAGTAATTA 907
Db 818 AAAATTTGCGGACAATGCTAAAAACCATAATAGTACAGCTGAATGAATCTGTAGAAATTA 877
QY 908 ATTGTACAAGACCCCAACAATACAAGAAAGGTTATCTATAGGACCAGGGAGAGCAT 967
Db 878 ATTGTACAAGACCCCAACAATACAAGAAAAAGTATACATATAGGACCAGGCAGAGCAT 937
QY 968 TTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTTAACATTAGTAGAG 1027
Db 938 TATATACAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTTAACCTTAGTAGAG 997
QY 1028 CAAAATGGAATAACACTTTACAACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATA 1087
Db 998 CAAAATGGAATGACACTTTAAATAAGATAGTTTATAAAATTAAGAGAACAAATTTGGGAATA 1057
QY 1088 AAACAATAGCCTTTAATCAATCCTCAGGAGGGGCCAGAAAAATTTGTAATGCACAGTTTTA 1147
Db 1058 AAACAATAGTCTTTAAGCATTCCTCAGGAGGGGCCAGAAAAATTTGTACGCGCACAGTTTA 1117
QY 1148 ATTGTGAGGGGAAATTCCTTCTACTGTTAATACAGCACAACTGTTTAATAGTACTTTGGAATG 1207
Db 1118 ATTGTGAGGGGAAATTTTCTACTGTAAATTCACACACAACTGTTTAATAGTACTTTGGAATG 1177
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QY 1388 GTA CTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAGATATGAGGGACAAATTGGA 1447
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QY 1448 GAAGTGAATTATATAAATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCCACCACCA 1507
Db 1415 GAAGTGAATTATATAAATATAAAGTAGTAAAAATTTGAACCATTAGGAGTAGCCACCACCA 1474
QY 1508 GGGCAAGAGAGAACAAGTGC AAAAGAGAAAAAGA 1542
Db 1475 AGGCAAGAGAGAAGAGTGGTGCAGAGAGAAAAAGA 1509
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RESULT 4  
US-10-728-195-7  
; Sequence 7, Application US/10728195  
; Publication No. US20040191269A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Shan  
; APPLICANT: Pal, Ranajit  
; APPLICANT: Kalyanaraman, V.S.  
; APPLICANT: Whitney, Stephen Charles  
; APPLICANT: Keen, Tim  
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN  
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS  
; FILE REFERENCE: 07917-269001

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; CURRENT APPLICATION NUMBER: US/10/728,195  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: US 60/430,732  
; PRIOR FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus  
US-10-728-195-7  
  
Query Match 58.2%; Score 1179.8; DB 18; Length 1422;  
Best Local Similarity 90.4%; Pred. No. 9.5e-264;  
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;  
  
QY 115 TTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAAGCAACCACCTCTATT 174  
Db 1 TTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCTCTATT 60  
  
QY 175 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGGCCACACATGCC 234  
Db 61 TGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGGCCACACATGCC 120  
  
QY 235 TGTGTACCCACAGACCCCAACCCACAAAGAGTAGTATTGGGAAATGTACAGAAAAATTT 294  
Db 121 TGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGAAAATGTGACAGAAAAATTT 180  
  
QY 295 AACATGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGAT 354  
Db 181 AACATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGAT 240  
  
QY 355 GAAAGCCTAAAGCCATGTGTAAAATTAAACCCCACTCTGTGTACTTTAAATTCGACTAAT 414  
Db 241 CAAAGCCTAAAGCCATGTGTAAAATTAACTCCACTCTGTGTACTTTAAATTCGACTGAT 300  
  
QY 415 TTGA-----ATATCACTAAGAATACTACTAATCCCACCTAGTAGCAGCTGGGAAATGATG 468  
Db 301 TTGAGGAATGCTACTAATGGGAATGACACTAATACCACCTAGTAGTAGGGAATGATG 360  
  
QY 469 GAGAAAGGAGAAATAAAAAAATGCTCTTTCTATATACCAAGCATACAGAAATAAGGTA 528  
Db 361 GGGGAGGAGAAATGAAAAAATGCTCTTTTCAAAATCACCACAAACATAAGAGGTAAGGTG 420  
  
QY 529 AAGAAAGAATATGCACCTTTTAAATAGACTTGTATGATGATGATACCAATAGAAAAATAC 588  
Db 421 CAGAAAGAATATGCACCTTTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAAT 480  
  
QY 589 ACTAAGTATAGGTTAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTA 648  
Db 481 AATAGATATAGGTTGATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGATA 540  
  
QY 649 TCCTTTCAGCCAAATCCCATACATTATTGTGTCCGGCTGGGTTTGGGATGCTAAAGTGT 708  
Db 541 TCCTTTGAGCCAAATCCCATACATTATTGTGCCCGGCTGGTTTTGGGATTCCTAAAGTGT 600  
  
QY 709 AACAAATAAGACATTCAATGGATCAGGACCATGCACAAATGTGAGCAGTACAAATGTACA 768  
Db 601 AAAGATAAGAAGTTCAATGGAAAAGGACCATTGTTCAAAATGTGAGCAGTACAAATGTACA 660  
  
QY 769 CATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAA 828  
Db 661 CATGGGATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAA 720  
  
QY 829 GACATAGTAATTAGATCTGAAAAATTTACAGACACAAATGCTAAAAACCATAATAGTACAGCTA 888  
Db 721 GAGGTAGTAATTAGATCCGAAAAATTTCCGGGACAAATGCTAAAAACCATAATAGTACAGCTG 780  
  
QY 889 AATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACATACAAGAAGAAAGGTTATCT 948  
Db 781 AATGAATCTGTAGAAATTAATTGTACAAGACCCCAACAACATACAAGAAGAAAGTATACAT 840  
  
QY 949 ATAGGACCGAGGAGAGCATTTTATGCAAGAAGAAACATAAATAGGAGATATAAGACAAGCA 1008
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Db      841 ATAGGACAGGCAGAGCATTTATATACAACAGGAGAAATAATAGGAGATATAAGACAAGCA 900
Qy      1009 CATTGTAACATTAGTAGAGCAAAATGGAATAAACACTTTTACAACAGATAGTTATAAAATTA 1068
Db      901 CATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTA 960
Qy      1069 AGAGAAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGACCCAGAA 1128
Db      961 AGAGAAACAATTTGGGAATAAAACAATAGTCTTTAAGCATTCCTCAGGAGGGACCCAGAA 1020
Qy      1129 ATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTTAATACAGCACAACTG 1188
Db      1021 ATTGTGACGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTTAATTCACACAACTG 1080
Qy      1189 TTTAATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATC 1248
Db      1081 TTTAATAGTACTTGGAAATGTTACTGAAGAGTCAAATAACACTGTAGAAAATAACACAATC 1140
Qy      1249 ACACCTCAATGCAGAAATAAAACAATTAATAATATGTGGCAGAAAAGTAGGAAAAGCAATG 1308
Db      1141 ACACCTCCATGCAGAAATAAAACAATTAATAACATGTGGCAGAAAAGTAGGAAGAGCAATG 1200
Qy      1309 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTA 1368
Db      1201 TATGCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTA 1260
Qy      1369 ACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGA 1428
Db      1261 ACAAGAGATGGTGGTCCAGAGGCAAAACA--AGACCGAGGTCTTCAGACCTGGAGGAGGA 1317
Qy      1429 GATATGAGGGACAAATTGGAGAGTGAAATTATATAATATAAAGTAGTAAGAAATTGAACCA 1488
Db      1318 GATATGAGGGACAAATTGGAGAGTGAAATTATATAATATAAAGTAGTAAGAAATTGAACCA 1377
Qy      1489 ATAGGAGTAGCACCCACCAGGCAAGGCAAGAGAAACAGTAGTCA 1529
Db      1378 TTAGGAGTAGCACCCACCAGGCAAGGCAAGAGAAAGAGTGGTGGA 1418
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RESULT 5
US-10-441-788-78/c
; Sequence 78, Application US/10441788
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/10/441,788
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/136,159A
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-10-441-788-78

Query Match      57.9%; Score 1174.2; DB 15; Length 3807;
Best Local Similarity 88.1%; Pred. No. 3e-262;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

Qy      52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111
Db      1668 TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609
Qy      112 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA 171
Db      1608 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAAAGAAAGCAACCACTCTA 1549
Qy      172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTGGGCCACACAT 231
Db      1548 TTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTGGGCCACACAT 1489
Qy      232 GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAAT 291
Db      1488 GCCTGTGTACCCACAGACCCCAACCCACAAGAGTAGAATTGGTAAATGTGACAGAAAAAT 1429
Qy      292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
Db      1428 TTTAACATGTGGAAAAATAACATGGTAGACAGATGCATGAGGATATAATCAGTTTATGG 1369
Qy      352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCACT 411
Db      1368 GATCAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTAAATTGCACT 1309
Qy      412 AATTG-----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGG 459
Db      1308 GATTGAGGAATACTACTAATACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGAG 1249
Qy      460 GGAATGATGGAGAAAGGAGAAATAAAAAATTGCTCTTCTCTATATCACCACAAGCATAGA 519
Db      1248 GGAACAATAAAGGGAGGAGAAATGAAAAAATGCTCTCTTCAATATCACCACAAGCATAGA 1189
Qy      520 AATAAGGTAAAGAAAGATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAAT 579
Db      1188 GATAAGATGCAGAAAGAAATATGCACCTCTTTATAAACTTGATATAGTATCAAT--AAAT 1132
Qy      580 ACTAATAATACTAAGTATAGGTTAATAAGTTGTAAACCTCAGTCATTACACAGGCCTGT 639
Db      1131 AATGATAGTACCAGCTATAGGTTGATAAGTTGTAAATACCTCAGTCATTACACAAGCTTGT 1072
Qy      640 CCAAAGGTATCCTTTCAGCCAATTCCTATACATATTATGTGTCCCGGCTGGTTCGCGATG 699
Db      1071 CCAAAGATATCCTTTGAGCCAATTCCTATACACTATTGTGCCCCGGCTGGTTCGCGATT 1012
Qy      700 CTAAAGTGTAACAATAAGACATTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTA 759
Db      1011 CTAAAGTGTAACGATAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTCAGCACAGTA 952
Qy      760 CAATGTACACATGGAAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAATGGCAGTCTA 819
Db      951 CAATGTACACATGGAAATTAGGCCAGTAGTATCAACTCAACTGCTGTAAATGGCAGTCTA 892
Qy      820 GCAGAAAGAGACATAGTAATTAGATCTGAAAAATTTTCAGACAATGCTAAAAACCATATA 879
Db      891 GCAGAAAGAGAGGTAGTAATTAGATCTGAGAATTTTCAATGATAATGCTAAAAACCATATA 832
Qy      880 GTACAGCTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATAACAAGAGA 939
Db      831 GTACATCTGAATGAATCTGTACAAATTAATTTGTACAAGACCCCAACTACAATAAAGAAA 772
Qy      940 AGGTTATCTATAGGACCAGGGAGAGCATTTTTTATGCAAGAAGAAACATAATAGGAGATATA 999
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Db 771 AGGATACATATAGGACCAGGAGAGCATTTTATACAAACAAAATATAATAGGAACTATA 712

Qy 1000 AGACAAGCACATTGTAAACATTAGTAGAGCAAAATGGAATAACACTTTTACAACACAGATAGTT 1059

Db 711 AGACAAGCACATTGTAAACATTAGTAGAGCAAAATGGAATGACACTTTTAAAGACAGATAGTT 652

Qy 1060 ATAAAAATTAAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGG 1119

Db 651 AGCAAAATTTAAAGAAACAATTTAAGAAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGG 592

Qy 1120 GACCCAGAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATACA 1179

Db 591 GACCCAGAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTCTTCTACTGTAAATCA 532

Qy 1180 GCACAACTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGACAAATGGCACTGAAGG--A 1236

Db 531 TCACCACACTGTTTAAATAGTACTTGGAAATGTTAATAATACTTGGAAATAATACTACAGGGTCA 472

Qy 1237 AATGACATAATCACACTCCAATGCAGAAATAAAACAATATATAATATGTGGCGAAGTA 1296

Db 471 AATAACAATATCACACTTCAATGCAAAATAAAACAATATAAACATGTGGCAGGAAGTA 412

Qy 1297 GGAAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACA 1356

Db 411 GGAAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA 352

Qy 1357 GGGTGCTACTAACAAAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTC 1413

Db 351 GGGTACTATTAAACAAGAGATGGTGGTAAGGACACGGGACACGAACGACACCGAGATCTTC 292

Qy 1414 AGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAGTGAATTATATAAATATAAAGTA 1473

Db 291 AGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAGTGAATTATATAAATATAAAGTA 232

Qy 1474 GTAAGAAATTGAACCAATAGGACTAGCACCCACCAGGGCAAGAGAAACACAGTGCAAAGA 1533

Db 231 GTAACAAATTGAACCAATTAGGACTAGCACCCACCACCAAGGCAAGAGAGTGTTGCAGAGA 172

Qy 1534 GAAAAAAGA 1542

Db 171 GAAAAAAGA 163

RESULT 6

US-09-966-931-27

; Sequence 27, Application US/09966931

; Publication No. US20030064361A1

; GENERAL INFORMATION:

; APPLICANT: Berman, Phillip W.

; Nakamura, Gerald R.

; TITLE OF INVENTION: HIV Envelope Polypeptides

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP

; STREET: 3 Embarcadero Center

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/966,931

; FILING DATE: 27-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/492,739

; FILING DATE: 2000-01-27

; ATTORNEY/AGENT INFORMATION:

; NAME: Haliday, Emily

; REGISTRATION NUMBER: 38903

; REFERENCE/DOCKET NUMBER: 14918-704

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-393-2000

; TELEFAX: 415-393-2286

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2552 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..2552

; SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-966-931-27

Query Match 57.8%; Score 1172.6; DB 10; Length 2552;

Best Local Similarity 89.2%; Pred. No. 5.8e-262;

Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

Qy 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAAATTTGGGGTC 123

Db 46 TGGGCGACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTGCAGAAAAAATTTGGGGTC 105

Qy 124 ACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACACCACCTCTATTTTGTGCATCA 183

Db 106 ACAGTCTATTATGGGGTACCTGTGTGGAAAGAGCAACACCACCTCTATTTTGTGCATCA 165

Qy 184 GATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 243

Db 166 GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCC 225

Qy 244 ACAGACCCCAACCCACAAGAAAGTAGTATTGGGAATGTGACAGAAAAATTTTAAATGTGG 303

Db 226 ACAGACCCCAACCCACAAGAAAAATAGGATTGGAAAAATGTAAACAGAAAAATTTTAAATGTGG 285

Qy 304 AAAAAATAACATGTTAGATCAGATGTCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA 363

Db 286 AAAAAATAACATGTTAGAACAGATGTCATGAGGATATAATCAGTTTATGGGATCAAAGCCTTA 345

Qy 364 AAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTTGAATATC 423

Db 346 AAGCCATGTGTAATAATTAACCCCACTATGTGTTACTTTAAATTCACATGATTG----- 399

Qy 424 ACTAAGAAATACTACTAATCCCACCTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA 483

Db 400 ---AAAAATGCTACTAATAACCACTAGTAGCAGCTGGGAAAGATGGAGAGAGGAGAAATA 456

Qy 484 AAAAAATTGCTCTTTCTATATACCAACAGCATAGAAATAAGGTAAAGAAAGAAATATGCA 543

Db 457 AAAAACTGCTCTTTTCAATGTCCACCAAGTATAAGAGATAAGATGAAGAAATGAATATGCA 516

Qy 544 CTTTTTAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTA 603

Db 517 CTTTTTTATAAACTTGATGTAGTACCAATAG---ATAATGATAATACTAGCTATAGGTTG 573

Qy 604 ATAAAGTTGTAAACACCTCAGTCATTAACAGGCCTGTCCAAAGGTATCCTTTTACGCCAATT 663

Db 574 ATAAAGTTGTAAACACCTCAGTCATTAACAGGCCTGTCCAAAGGTGTCTCTTTGAGCCAATT 633

Qy 664 CCCATACATTATTGTGTCCCGGCTGGGTTTCGGATGCTTAAAGTGTAAACAATAAGACATTTC 723

Db 634 CCCATACATTATTGTGTCCCGGCTGGTTCGGATTCTTAAAGTGTAGAGATAAAAAGTTTC 693

Qy 724 AATGGATCAGGACCATGCACAAATGTCCAGCACAGTACATGTACACATGGAATTAGGCCA 783

Db 694 AACGGAAACAGGACCATGTACAAATGTCCAGCACAGTACAAATGTACACATGGAATTAGGCCA 753

Qy 784 GTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTTAGCAGAAAGACATAGTAATTAGA 843

Db	754	GTAGTATCAACTCACTGCTGTTAAATGGCAGTTTAGCAGAAGAAGTAGTAAATTAGA	813
QY	844	TCTGAAAAATTTTCACAGACAATGCTAAAAACCATATAATAGTACAGCTAAATGAATCTGTAGTA	903
Db	814	TCTGCCAAATTTCTCGGACAAATGCTAAAAACCATATAATAGTACAGCTGAAACGAATCTGTAGAA	873
QY	904	ATTAATTGTACAAGACCCCAACAACAATAACAAGAGAAGGTTATCTATAGGACCAAGGGAGA	963
Db	874	ATTAATTGTACAAGACCCCAACAACAATAACAAGAGAAGTATACATATAGGACCAAGGGAGA	933
QY	964	GCATTTTATGCAAGAAGAAAAATAATAGGAGATATAAGACAAGCACATTGTAAACATTAGT	1023
Db	934	GCATTTTATGCAACAGGAGAAAAATAATAGGAGACATAAGACAAGCACATTGTAAACCTTAGT	993
QY	1024	AGAGCAAAATGGAATAACACACTTTACAACAGATAGTTATAAAAAATTAAGAGAAAAATTTAGG	1083
Db	994	AGCACAAAATGGAATAATACTTTAAAAACAGATAGTTACAAAATTAAGAGAACATTTT---	1050
QY	1084	AATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCAGAAAAATTGTAATGCACAGT	1143
Db	1051	AATAAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCCAGAAAAATTGTAATGCACAGT	1110
QY	1144	TTTAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTGG	1203
Db	1111	TTTAATTGTGGAGGGGAATTTTCTACTGTAATACAAACCACTGTTTAAATAGTACTTGG	1170
QY	1204	AATGTTACTGGAGGGACAAAATGGCACTGAAGGAAATGA-----CATAAATCACA	1251
Db	1171	AATTATACTTATACTTGGAAATAATACTGAAGGTCAAAATGACACTGGAAAGAAATATCACA	1230
QY	1252	CTCCAATGCAGAAATAAAAACAAAATTTATAAATATGTGGCAGAAAAAGTAGGAAAAAGCAATGTAT	1311
Db	1231	CTCCAATGCAGAAATAAAAACAAAATTTATAACATGTGGCAGGAAGTAGGAAAAAGCAATGTAT	1290
QY	1312	GCCCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACA	1371
Db	1291	GCCCCCTCCCATAGAGGACAAAATTAGATGCTCATCAAAATATTACAGGGCTGCTATTAAACA	1350
QY	1372	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT	1431
Db	1351	AGAGATGGTGGTAATA-----ACAGCGAAACCCGAGATCTTCAGACCTGGAGGAGGAGAT	1404
QY	1432	ATGAGGGACAAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGAAATTGAACCAATA	1491
Db	1405	ATGAGGGACAAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTTGAACCATTA	1464
QY	1492	GGAGTAGCACCCACCAAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAAGACCCG	1546
Db	1465	GGAGTAGCACCCACCAAGGGCAAGAGAGAGAGTGTATGACAGAGAGAAAAAAGAGCAG	1519

## RESULT 7

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US-10-459-121-27
; Sequence 27, Application US/10459121
; Publication No. US20040121317A1
; GENERAL INFORMATION:
;   APPLICANT: Berman, Phillip W.
;             Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
;   STREET: 3 Embarcadero Center
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94111
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEO for Windows Version 2.0

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Db 877 CTGAATGAATCTGTACAAATTAAATTGTACAGACCCCACTACAATAAAGAAAAAGGATA 936  
Qy 946 TCATATAGGACAGGGAGAGCATTTTATGCAAGAAGAAAACATAATAGGAGATATAAGACAA 1005  
Db 937 CATATAGGACAGGGAGAGCATTTTATACAAACAAAATAATAATAGGAACATAAGACAA 996  
Qy 1006 GCACATTGTAAACATTAGTAGCAAAAATGGAATAACACATTACAAACAGATAGTTATAAAA 1065  
Db 997 GCACATTGTAAACATTAGTAGCAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056  
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGACCCA 1125  
Db 1057 TTAAGAGAAAAATTTAAGAAATAAAACAATAGTCTTTTAATCAATCCTCAGGAGGGACCCA 1116  
Qy 1126 GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTACTGTAATACAGCAAA 1185  
Db 1117 GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATACATACCA 1176  
Qy 1186 CTGTTTAATAGTACTTGAATG---TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242  
Db 1177 CTGTTTAATAGTACTTGAATGTAATAATACTTGGAAATAATACTACAGGGTCAATAAC 1236  
Qy 1243 ATAATCACACTCCAATGCAGATAAAACAAATTATAAATATGTGGCAGAAAAGTAGGAAA 1302  
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTATAAACAATGTGGCAGGAAGTAGGAAA 1296  
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG 1362  
Db 1297 GCAATGTATGCCCTCCCATTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356  
Qy 1363 CTACTAAACAAGAGATGGAGGTAATAGTAGTGA---GACTGAGACTGAGATCTTCAGACCT 1419  
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGGACACGACACCGAGATCTTCAGACCT 1416  
Qy 1420 GGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAGA 1479  
Db 1417 GGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAACA 1476  
Qy 1480 ATTGAACCAATAGGAGTAGCACCACCAGGGCAAAGAGAGAAACAGTGCAAAGAGAAAAA 1539  
Db 1477 ATTGAACCAATTAGGAGTAGCACCACCAGGCAAAGAGAGAGTGGTGCAGAGAGAAAAA 1536  
Qy 1540 AGACCGGATCCAGAA 1554  
Db 1537 AGACGAGCGATAGGA 1551

RESULT 9

US-10-077-294-3  
; Sequence 3, Application US/10077294  
; Publication No. US20020159979A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R.  
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/077,294  
; FILING DATE: 15-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/691,604  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020159979Aland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31975  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2571 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-077-294-3  
  
Query Match 57.8%; Score 1172.2; DB 13; Length 2571;  
Best Local Similarity 87.9%; Pred. No. 7.2e-262;  
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;  
  
Qy 58 TCGGCTTCGAGATCCATGCTCTCTTGGGATATTGATGATCTGTAGTACAGAAAAATTG 117  
Db 40 TGGGGATGGGCACGATGCTCTTGGGTTATTAATGATCTGTAGTCTACAGAAAAATTG 99  
Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAACACCACCTCTATTTTGT 177  
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAACACCACCTCTATTTTGT 159  
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGCCACACATGCCTGT 237  
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGCCACACAGCCTGT 219  
Qy 238 GTACCCACAGACCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAAC 297  
Db 220 GTACCCACAGACCCCAACCCACAAGAGTAGAATTGGTAAATGTGACAGAAAAATTTTAAAC 279  
Qy 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357  
Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339  
Qy 358 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTTAAATGCACTAATTG 417  
Db 340 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTTACTTTTAAATGCACTGATTG 399  
Qy 418 -----AATATCACTAAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465  
Db 400 AGGAATACTACTAATAACCAATAATAGTAGTCTGCTAATAACAATAAGTAGTAGCGAGGGAACA 459  
Qy 466 ATGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATACCCACAAGCATAAAGAAATAAG 525  
Db 460 ATAAAGGGAGGAGAAATGAAAAACTGCTCTTTCAATATACCCACAAGCATAAAGAGATAAG 519  
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATACTAAT 585  
Db 520 ATGCAGAAAGAAATATGCACCTCTTTATAAACTTTGATATAGTATCAATAG--ATAATGAT 576  
Qy 586 AATACTAAGTATAGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCCTGTCCCAAG 645  
Db 577 AGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAAGCTTTGTCCAAAG 636  
Qy 646 GTATCCTTTCAGCCCAATTCCCATACATTATTGTGTCGGGTGGGTTTGCATGCTAAAG 705  
Db 637 ATATCCTTTGAGCCCAATTCCCATACACTATTGTGCCCCGGCTGGTTTTCGATTCTAAAAA 696  
Qy 706 TGTAACAAATAAGACATTCAATGGATCAGGACCATGCACAAATGTGACACAGTACAAATGT 765  
Db 697 TGTAACGATAAAAAGTTCAAGTGGAAGGATCATGTAAAAATGTGACGACAGTACATGT 756  
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 825



QY	646	GTATCCTTTTCAGCCAATTC	CCCATACATATTGTGTGCCGGCTGGTTTGC	GATGCTAAAG	705	
DB	637	ATATCCTTTTGAGCCAATTC	CCCATACACTATTGTGCCCCGGCTGGTTTGC	GATTCTAAAA	696	
QY	706	TGTAACAATAAGACATTC	CAATGGATCAGGACCATG	CACAAAATGT	CAGCACAGTACAATGT	765
DB	697	TGTAACGATAAAAAAGTT	CAGTGGAAGGATCATGT	AAAAAATGT	CAGCACAGTACAATGT	756
QY	766	ACACATGGAATTAGSCCAGT	GGTGTCAACTCAACTGCT	GTAAATGGCAGTCT	TAGCAGAA	825
DB	757	ACACATGGAATTAGSCCAGT	AGTATCAACTCAACTGCT	GTAAATGGCAGTCT	TAGCAGAA	816
QY	826	GAAGACATAGTAATTAGAT	CTGAAAAATTTCA	CAGACAATGCT	AAAAACCAATAATAGTACAG	885
DB	817	GAAGAGGTAGTAATTAGAT	CTGAGAAATTTCACTG	ATAATGCTAAAAACCATCATAGTACAT	876	
QY	886	CTAAATGAATCTGTAGTA	ATAATTGTACAAGACCCAA	CAAAATACAAAGAAGAGGTTA	945	
DB	877	CTGAATGAATCTGTACAAA	TTAATTGTACAAGACCCAACT	ACAACTACAAATAAAAGAAAAGGATA	936	
QY	946	TCTATAGGACCCAGGAGAG	CATTTTATGCAAGAGAAAA	CATAATAGGAGATATAAGACAA	1005	
DB	937	CATATAGGACCCAGGAGAG	CATTTTATACAACAAAAA	TATAATAGGAACATAAGACAA	996	
QY	1006	GCACATTGTAACATTAGT	AGACAAAATGGATAACACT	TTTACAACAGATATGTTATAAAA	1065	
DB	997	GCACATTGTAACATTAGT	AGACAAAATGGAAATGACACT	TTTAAGACAGATAGTTAGCAAA	1056	
QY	1066	TTAAGAGAAAAATTTAG	GAATAAAACAATAGCCT	TTAAATCAATCCTCAGGAGGGACCCA	1125	
DB	1057	TTAAAAGAACAAATTTA	AGAATAAAACAATAGCT	TTTAATCAATCCTCAGGAGGGACCCA	1116	
QY	1126	GAATTTGTAATGCACAGT	TTTAAATTGTGGAGGGAAT	TTCTTCTACTGTATAACAGCACAA	1185	
DB	1117	GAATTTGTAATGCACAGT	TTTAAATTGTGGAGGGAAT	TTTTTCTACTGTATAACATCACCA	1176	
QY	1186	CTGTTTAATAGTACTTGG	AATG--TTACTGGAGGACAAAT	GGCACTGAAGGAATGAC	1242	
DB	1177	CTGTTTAATAGTACTTGG	AATGGTAATAACTTTGGAATAATA	CTACAGGGTCAAAATAAC	1236	
QY	1243	ATAATCACACTCCAATGC	AGAATAAAACAAATTTATAAATAT	GTGGCAGAAAGTAGGAAAA	1302	
DB	1237	AATATCACACTTCAATGC	AAAAATAAAACAAATTTATAAACAT	GTGGCAGGAAGTAGGAAAA	1296	
QY	1303	GCAATGTATGCCCCCTCC	ATCAGGACAAATTAGATGTT	TCATCAAAATATTACAGGGCTG	1362	
DB	1297	GCAATGTATGCCCCCTCC	ATTTGAAGGACAAATTAGATGTT	TCATCAAAATATTACAGGGCTA	1356	
QY	1363	CTACTAACAGAGATGG	AGGTAATAGTACTGA--GACTG	GAGCTGAGATCTTCAGACCT	1419	
DB	1357	CTATTACAGAGATGGT	GGTAAGGACACGGACACGAAC	CGACCCGAGATCTTCAGACCT	1416	
QY	1420	GGAGGAGGAGATATGAG	GGACAATTTGGAGAAGTGAAT	TATATAAATATAAAGTAGTAAGA	1479	
DB	1417	GGAGGAGGAGATATGAG	GGACAATTTGGAGAAGTGAAT	TATATAAATATAAAGTAGTAACA	1476	
QY	1480	ATTGAACCAATAGGAGT	AGCACCACCGGGCAAAGAGA	GAACAGTGC	AAAGAGAAAAA	1539
DB	1477	ATTGAACCAATTAGGAGT	AGCACCACCGCAAAGAGA	GAGTGGTGC	AGAGAGAAAAA	1536
QY	1540	AGACCGGATCCAGAA	1554			
DB	1537	AGAGCAGCGATAGGA	1551			

340 AGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAATTCACCTGATTTG 399

418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465

400 AGGAATACTACTAATACCAATAATAGTAGTCTGCTAATAACAATAGTATAGCGAGGGAACA 459

466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAAGCATAGAAATAAG 525

RESULT 11  
US-10-263-127-3  
; Sequence 3, Application US/10263127  
; Publication No. US20030082145A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Philip R  
; TITLE OF INVENTION: Adeno-As  
; Methods



Db	460	ATAAAGGAGGAGAAATGAAAAA	CTGCTCTTTCAATATCACCACAAGCATAGAGATAAG	519
QY	526	GTAAAGAAAGAATATGCAC	TTTTTAATAGACTTTGATGTAGTACCAATAGAAAACTAATA	585
Db	520	ATGCAGAAAGAATATGCAC	TTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT	576
QY	586	AATACTAAGTATAGGTTAA	TAAAGTTGTAACACCTCAGTCATTACACAGGCGCTGTCCAAAG	645
Db	577	AGTACCAGCTATAGGTTGA	TAAAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAAG	636
QY	646	GTATCCTTTTCAGCCAA	TTCCTCCATACATTTATTGTGTCCGGCTGGGTTTGGCATGCTAAAG	705
Db	637	ATATCCTTTGAGCCA	ATTTCCCATACACTATTGTGCCCCGGCTGGTTTTCGATTTCTAAAA	696
QY	706	TGTAACAATAAGACAT	TCAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAATGT	765
Db	697	TGTAACGATAAAAA	AGTTTCAGTGGAAAAGGATCATGTAAAAATGTGAGCACAGTACAATGT	756
QY	766	ACACATGGAATTAGGCC	AGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA	825
Db	757	ACACATGGAATTAGGCC	AGTAGTATCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA	816
QY	826	GAAGACATAGTAATTAG	ATCTGAAAAATTTTCACAGACAATGCTAAAAACCAATAATAGTACAG	885
Db	817	GAAGAGGTAGTAATTAG	ATCTGAGAAATTTCACTGATAATGCTAAAAACCATCATAGTACAT	876
QY	886	CTAAATGAATCTGTAG	TAATTAATTGTACAAGACCCAAACAATAACAGAAAGGTTTA	945
Db	877	CTGAATGAATCTGTACA	AAATTAATTGTACAAGACCCAACTACAATAAAAGAAAAAGGATA	936
QY	946	TCTATAGGACCGGAG	AGCATTTTATGCAAGAAGAAAAACATAATAGGAGATATAAGACAA	1005
Db	937	CATATAGGACCGGAG	AGCATTTTATACAACAAAAATATAATAGGAATATAAGACAA	996
QY	1006	GCACATTGTAACATTAG	TAGAGCAAAATGGAATTAACACTTTTACAACAGATAGTTATAAAA	1065
Db	997	GCACATTGTAACATTAG	TAGAGCAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA	1056
QY	1066	TTAAGAGAAAAATTTAG	GAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA	1125
Db	1057	TTAAAGAAACAATTTA	AGAAATAAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA	1116
QY	1126	GAAATTGTAATGCAC	AGTTTAAATTTGTGGAGGGAAATCTTCTACTGTAATACAGCACAA	1185
Db	1117	GAAATTGTAATGCAC	AGTTTAAATTTGTGGAGGGAAATTTTCTACTGTAATACATCACCA	1176
QY	1186	CTGTTTAATAGTACT	TTGGAATG--TTACTGGAGGGAACAATGGCACTGAAGGAAATGAC	1242
Db	1177	CTGTTTAATAGTACT	TTGGAATGGAATAATACTTGGAAATAATACTACAGGGTCAATAAAC	1236
QY	1243	ATAATCACACTCCA	ATCGAGAATAAAAACAAAATTAATAATATGTGGCAGAAAAGTAGGAAAA	1302
Db	1237	AATATCACACTTCA	ATGCAAAATAAAAACAAAATTAATAACATGTGGCAGGAAGTAGGAAAA	1296
QY	1303	GCAATGTATGCCCC	TCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTG	1362
Db	1297	GCAATGTATGCCCC	TCCCATTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTA	1356
QY	1363	CTACTAACAGAGAT	TGGAGTAAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT	1419
Db	1357	CTATTAAACAAGAG	ATGGTGGTAAGGACACGGACACGACCGAGATCTTCAGACCT	1416
QY	1420	GGAGGAGGAGATATG	AGGACAAATTTGGAGAAAGTGAATTAATAAAATATAAAGTAGTAAGA	1479
Db	1417	GGAGGAGGAGATATG	AGGACAAATTTGGAGAAAGTGAATTAATAAAATATAAAGTAGTAACA	1476
QY	1480	ATTGAACCAATAGG	AGTAGCACCCACCGGGCAAGAGAGAAACAGTGCAAAGAGAGAAAA	1539
Db	1477	ATTGAACCAATTAGG	AGTAGCACCCACCGGGCAAGAGAGAGTGGTGCAGAGAGAGAAAA	1536
QY	1540	AGACCGGATCCAG	AA	1554

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Db      1537 AGAGCAGCGATAGGA 1551

RESULT 12
US-10-375-777-3
; Sequence 3, Application US/10375777
; Publication No. US20030147912A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; Methods
;
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,777
; FILING DATE: 26-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030147912Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-375-777-3

Query Match      57.8%; Score 1172.2; DB 15; Length 2571;
Best Local Similarity 87.9%; Pred. No. 7.2e-262;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4

QY      58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117
Db      40 TGGGGATGGGGCACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99

QY      118 TGGGTCACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 177
Db      100 TGGGTCACAGTCTATTATGGGTACCTGTGTGGAAAGAGCAACCACTCTATTTTGT 159

QY      178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGT 237
Db      160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219

QY      238 GTACCCACAGACCCCAACCCACAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
Db      220 GTACCCACAGACCCCAACCCACAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAC 279

QY      298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357

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Db 280 ATGTGGAATAAATGATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339

Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATAATTG 417

Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTAAATTGCACATGTTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465

Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAATAGCGAGGGAACA 459

Qy 466 ATGAGAAAGGAGAAATAAAATAATTGCTCTTTCTATATACCAACAAGCATAAAGAAATAAG 525

Db 460 ATAAAGGAGGAGAAATGAAAAAAGTCTCTTTCAATATATCAACAAGCATAAAGAGATAAG 519

Qy 526 GTAAAGAAAGAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAAT 585

Db 520 ATGCAGAAAGAATATGCACCTTCTTTATATAAACTTGATATAGTATCAATAG---ATAATGAT 576

Qy 586 AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTAACAGGCCCTGTCCAAAG 645

Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTTCAGTCATTACACAAGCTTGTCCAAAG 636

Qy 646 GTATCCTTTTCAGCCAAATCCCATACATTATTGTGTCCCGGCTGGGTTTGGCATGCTAAAG 705

Db 637 ATATCCTTTGAGCCAAATCCCATACACTATTGTGCCCGGCTGGTTTGGGATTTCTAAAA 696

Qy 706 TGTAAACAATAAGACATTCAATGGATCAGGACCATGCAAAATGTCAGCACAGTACAATGT 765

Db 697 TGTAACGATAAAAAGTTTCAGTGGAAGAAGGATCATGTAAAAATGTCAGCACAGTACAATGT 756

Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAA 825

Db 757 ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAA 816

Qy 826 GAAACATAGTAATTAGATCTGAAAAATTTCACAGACAAATGCTAAAAACCATAATAGTACAG 885

Db 817 GAAAGGTAGTAATTAGATCTGAGAAATTTCACCTGATAATGCTAAACCATCATAGTACAT 876

Qy 886 CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAGAAGTTA 945

Db 877 CTGAATGAATCTGTACAAATTAATTGTACAAGACCCCACTACAATAAAGAAAAAGGATA 936

Qy 946 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 1005

Db 937 CATATAGGACCGGAGAGCATTTTATACAACAAAAAATATAATAGGAACTATAAGACAA 996

Qy 1006 GCACATTGTAACATTAGTAGACAAAAATGGAATAACACTTTTACAACAGATAGTTATAAAA 1065

Db 997 GCACATTGTAACATTAGTAGACAAAAATGGAATGACACTTTAAGACAGATAGTTAGCAAA 1056

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Db 1117 GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176

Qy 1186 CTGTTTAATAGTACTTTGGAATG---TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242

Db 1177 CTGTTTAATAGTACTTTGGAATGGTAATAATACTTGGAAATAATACTACAGGGTCAATAAC 1236

Qy 1243 ATAATCACACTCCCAATCGAATAAAAAAATAATTATAAATATGTGGCAGAAAGTAGGAAAA 1302

Db 1237 AATATCACACTTCAATGCAAAATAAAAAAATAATTATAAATGTTGGCAGGAAGTAGGAAAA 1296

Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCAATCAAAATATTACAGGGCTG 1362

Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCAATCAAAATATTACAGGGCTA 1356

Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419

Db 1357 CTATTAAACAAGAGATGGTGTAAAGGACACGGACACGAAACGACACCGAGATCTTCAGACCT 1416

Qy 1420 GGAGGAGGAGATATGAGGACAATTTGGAGAAAGTGAATTTATATAAAATATAAAGTAGTAAGA 1479

Db 1417 GGAGGAGGAGATATGAGGACAATTTGGAGAAAGTGAATTTATATAAAATATAAAGTAGTAACA 1476

Qy 1480 ATTGAACCAATAGGAGTAGCACCCCAAGGGCAAAAGAGAAGAACAGTGCAAAAGAGAAAAA 1539

Db 1477 ATTGAACCATTAGGAGTAGCACCCCAAGGCAAAAGAGAAGAGTGGTGCAGAGAGAAAAA 1536

Qy 1540 AGACCGGATCCAGAA 1554

Db 1537 AGACGAGCGATAGGA 1551

RESULT 13

US-10-351-938-3

; Sequence 3, Application US/10351938

; Publication No. US20040009603A1

; GENERAL INFORMATION:

; APPLICANT: Oxford Biomedica (UK) Limited

; TITLE OF INVENTION: Anti-Viral Vectors

; FILE REFERENCE: 674524-2004

; CURRENT APPLICATION NUMBER: US/10/351,938

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: US/09/552,950

; PRIOR FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2571

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-10-351-938-3

Query Match 57.8%; Score 1172.2; DB 16; Length 2571;

Best Local Similarity 87.9%; Pred. No. 7.2e-262;

Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTG 117

Db 40 TGGGGATGGGGCACGATGCTCCTTGGGTATTAAATGATCTGTAGTCTACAGAAAAATTG 99

Qy 118 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAAGCAACCACCTCTATTTTGT 177

Db 100 TGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCTCTATTTTGT 159

Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAAATGTTTGGCCACACATGCCTGT 237

Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAAATGTTTGGCCACACAGCCTGT 219

Qy 238 GTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAAC 297

Db 220 GTACCCACAGACCCCAACCCACAAGAAGTAGAATTGGTAAATGTGACAGAAAAATTTAAAC 279

Qy 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357

Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339

Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTTGCACATAATTG 417

Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTTACTTTTAAATTTGCACATTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATG 465

Db 400 AGGAATACTACTAATAACCAATAATAGTACTGCTAAACAATAAGTAATAGCGAGGGAACA 459

Qy 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTCTATATCACCAAGCATAAAGAAATAAG 525

Db 460 ATAAAGGAGGAGAAATGAAAAAAGTCTCTCTTCAATATCACCAAGCATAAAGAGATAAG 519

Qy 526 GTAAAGAAAGAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAAT 585

Db 520 ATGCAGAAAGAATATGCACCTTCTTTTATAAACTTTGATATAGTATCAATAG---ATAATGAT 576







D <b>b</b>	166	GATGCTAAAGCATATGATACAGAGATAACAATAATGTTTGGGCCACACATGCCTGTGTACCC	225
Q <b>y</b>	244	ACAGACCCCACCAACAAGAAGTAGTATTGGGAATGTGACAGAAAAATTTTAACCATGTGG	303
D <b>b</b>	226	ACAGACCCCACCAACAAGAAGTAGTATTGGAAAATGTGACAGAAAAATTTTAACCATGTGG	285
Q <b>y</b>	304	AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
D <b>b</b>	286	AAAAATAACATGGTGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGTTTA	345
Q <b>y</b>	364	AAGCCATGTGTAAAAATTAACCCCCACTCTGTGTACTTTAAATTGCACATAATTTGAATATC	423
D <b>b</b>	346	AAGCCATGTGTAAAAATTAACCCCCACTCTGTGTACTTTAAATTGCACATGAT-----	396
Q <b>y</b>	424	ACTAAGAATACTACTAATCCCACTAGTAGAGCTGGGGAATGATGGAGAAGGAGAAAAATA	483
D <b>b</b>	397	GCGGGGAATACTACTAATAACCAATAGTAGTAGCAGGGAAAAAGCTGGAGAAGGAGAAAAATA	456
Q <b>y</b>	484	AAAAATTGCTCTTTCTATATCACCCACCAAGCATAAAGATAAGGTAAGAAAGAAATATGCA	543
D <b>b</b>	457	AAAAACTGCTCTTTCAATATCACCCAAGCGTGAGAGATAAGATGCAGAAAAGAAACTGCA	516
Q <b>y</b>	544	CTTTTTTAATAGACTTGATGTAGTACCATAAGA-----AAATACTAAT	585
D <b>b</b>	517	CTTTTTTAATAAACCTGATATAGTACCAATAGATGATAGGAATAGTACTAGGAAT	576
Q <b>y</b>	586	AATACTAAGTATAGGTTAATAAGTTGTAACACTCAGTCATTACACAGGCTGTCCAAAG	645
D <b>b</b>	577	AGTACTAACTATAGGTTGATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAG	636
Q <b>y</b>	646	GTATCCTTTTCAGCCAATTCCCATAACATATTGTGTCCGGCTGGTTTGGCATGCTAAAG	705
D <b>b</b>	637	GTATCATTTTGAGCCAATTCCCATAACATTTCTGTACCCCGGCTGGTTTGGCTTCTAAAG	696
Q <b>y</b>	706	TGTAACAATAAGACATTTCAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAATGT	765
D <b>b</b>	697	TGTAATAATAAGACGTTCAATGGATCAGGACCATGCAAAAAATGTGAGCACAGTACAATGT	756
Q <b>y</b>	766	ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	825
D <b>b</b>	757	ACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA	816
Q <b>y</b>	826	GAAGACATAGTAATTAGATCTGAAAAATTCACAGACAATGCTAAAAACCAATAATAGTACAG	885
D <b>b</b>	817	GGAGAGGTAGTAATTAGATCTGAAAAATTCACGNAACAATGCTAAAAACCAATAATAGTACAG	876
Q <b>y</b>	886	CTAAATGAATCTGTAGTAATTAATTGTACAAGACCCCAACAACAATACAAGAAAGGTTA	945
D <b>b</b>	877	CTGACAGAACCCAGTAAAAATTAATTGTACAAGACCCCAACAACAATACAAGAAAAAGTATA	936
Q <b>y</b>	946	TCTATAGGACCGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAA	1005
D <b>b</b>	937	CCTATAGGACCGGAGAGCATTTTATGCAACAGGAGACATAATAGGAATATAAGACAA	996
Q <b>y</b>	1006	GCACATTGTAACATTAGTAGAGCAAAATGGAATPAACACTTTACAACAGATAGTTATAAAA	1065
D <b>b</b>	997	GCACATTGTAACCTTAGTAGAAGACAGACTGGAATAACACTTTAGGACAGATAGTTGAAAAA	1056
Q <b>y</b>	1066	TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCCTCAGGAGGGACCCA	1125
D <b>b</b>	1057	TTAAGAGAACAAATTTGGGAATAAAACAATAATCTTTAATCACTCCTCAGGAGGGACCCA	1116
Q <b>y</b>	1126	GAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAA	1185
D <b>b</b>	1117	GAAATTGTAATGCACAGTTTAAATTGTAGAGGGGAATTTTCTACTGTAATACACACAA	1176
Q <b>y</b>	1186	CTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGACAAATG-----GCACTGAAGGAAAT	1239
D <b>b</b>	1177	TTGTTTGACAGTACTTGGGATAAATACTAAAGTGTCAAATGGCACTAGCACTGAAGAGAAT	1236
Q <b>y</b>	1240	GACATAATCACACTCCAATGCAGAATAAAACAATTTATAAATATGTGGCAGAAAGTAGGA	1299

Db	1237	AGCACAATCACACTCCCATGCAGAAATAAAGCAAATTTGTAACATGTGGCAGGAAGTAGGA	1296
Qy	1300	AAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGG	1359
Db	1297	AAAGCAATGTATGCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAAATATTACAGG	1356
Qy	1360	CTGCTACTAACAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCT	1419
Db	1357	TTGCTATTAACAAGAGATGGAGG---TAGTTAAACAAGCATGAATGAGACCTTCAGACCT	1413
Qy	1420	GGAGGAGGAGATATGAGGACAAATTGGAGAA GTGAATTATATAAAATATAAAGTAGTAAGA	1479
Db	1414	GGAGGAGGAGATATGAGGACAAATTGGAGAA GTGAATTATACAAATATAAAAGTAGTAAA	1473
Qy	1480	ATTGAACCAATAGGAGTAGCACCCACCAGGGCAAGAGAAAGAACAGTGCAAAAGAGAAAA	1539
Db	1474	ATTGAACCAATTAGGAGTAGCACCCACCAGGGCAAGAGAAAGAGTGGTGCAGAGAGAAAA	1533
Qy	1540	AGACCGG	1546
Db	1534	AGAGCAG	1540

Search completed: November 12, 2004, 19:50:40  
Job time : 712.358 secs





Db 292 ATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGAT 351

QY 1582 CAGAATCCTCAAAATTCGGCACATGTCATAAGTGAGGCAGCAGTAAACAAACATCTGTG 1641

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Db 472 GGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC 531

QY 1762 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCC 1821

Db 532 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCC 591

QY 1822 CCCGGTAGATTCGAGAGAACTTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCT 1881

Db 592 CCCGGTAGATTCGAGAGAACTTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCT 651

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Db 652 TCGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTG 711

QY 1942 TTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGC 2001

Db 712 TTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGC 771

QY 2002 TTAICTCAAACCTC 2013

Db 772 TTAICTCAAACCTC 783

RESULT 2

AY416062

LOCUS

DEFINITION Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY416062

VERSION AY416062.1 GI:39772022

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 786)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 786)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

1..786

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

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ORIGIN

/locus\_tag="HCM5765"

Query Match 22.9%; Score 464.8; DB 9; Length 786;

Best Local Similarity 96.5%; Pred. No. 5.8e-104;

Matches 475; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1522 ACAGTGCAAGAGAGAAAAAGACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGAT 1581

Db 292 ATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGAT 351

QY 1582 CAGAATCCTCAAAATTCGGGCACATGTCTATAAGTGAGGCAGCAGTAAACAAACATCTGTG 1641

Db 352 CAGAATCCTCAAAATTCGGGCACATGTCTATAAGTGAGGCAGCAGTAAACAAACATCTGTG 411

QY 1642 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAAT 1701

Db 412 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAAT 471

QY 1702 GGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC 1761

Db 472 GGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC 531

QY 1762 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCC 1821

Db 532 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCC 591

QY 1822 CCCGGTAGATTCGAGAGAACTTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCT 1881

Db 592 CCCGGTAGATTCGAGAGAACTTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCT 651

QY 1882 TCGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTG 1941

Db 652 TCGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTG 711

QY 1942 TTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGC 2001

Db 712 TTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGC 771

QY 2002 TTAICTCAAACCTC 2013

Db 772 TTAICTCAAACCTC 783

RESULT 3

CD638712

LOCUS

DEFINITION CD638712 767 bp mRNA linear EST 17-JUN-2003

AGENCY AGENCOURT 14532410 NIH MGC\_191 Homo sapiens cdna clone

IMAGE:30416146 5', mRNA sequence.

ACCESSION CD638712

VERSION CD638712.1 GI:31804800

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 767)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: NDCM215 row: h column: 11



LOCUS CD521613 806 bp mRNA linear EST 06-JUN-2003  
DEFINITION AGENCOURT\_14356206 NIH\_MGC\_191 Homo sapiens cDNA clone  
IMAGE:30413128 5', mRNA sequence.  
ACCESSION CD521613  
VERSION CD521613.1 GI:31453331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 806)  
NIH-MGC http://mgc.nci.nih.gov/.  
REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)  
AUTHORS Unpublished (1999)  
TITLE Contact: Daniela S. Gerhard, Ph.D.  
JOURNAL Office of Cancer Genomics  
COMMENT National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDCM207 row: j column: 17  
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/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed  
and directionally cloned. PBMC - Peripheral Blood  
Mononuclear Cells. RNA was pooled from 3/6hour stimulation  
with PMA adn Ionomycin. 5' and 3' adaptors were used in  
cloning as follows: 5' adaptor sequence:  
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGGCGGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.69  
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 16.1%; Score 327; DB 6; Length 806;  
Best Local Similarity 91.5%; Pred. No. 8.1e-70;  
Matches 356; Conservative 0; Mismatches 32; Indels 1; Gaps 1;  
QY 1522 ACAGTGCAAAGAGAAAAAGACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGAT 1581  
DB 386 ATAATGTTAAACAAGAGGAGACGAAGAAGANAACAGCTTTGAAATGCAAAAAGGTGAT 445  
QY 1582 CAGAACTCCTCAAAATTGCGGCACATGTCTATAAGTGAGGCCAGCAGTAAACAACATCTGTG 1641  
DB 446 CAGAACTCCTCANATTGCGGCACATGTCTATAAGTGAGGCCAGCAGTAAACAACATCTGTG 505  
QY 1642 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAAT 1701  
DB 506 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAAT 565  
QY 1702 GGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTATATCTATATGCCCCAAGTCACCTTC 1761  
DB 566 GGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTATATCTATATGCCCCAAGTCACCTTC 625  
QY 1762 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCC 1821

DB 626 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCCTTAAAGTCC 685  
QY 1822 CCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCT 1881  
DB 686 CCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCCAAGTTCGCGCAAAACCT 745  
QY 1882 T-GCGGGCAACAATCCATTCACTTTGGGAG 1909  
DB 746 TGGCGGGCAACAATCCCTTTCCCTTGGGG 774  
CN794193 571 bp mRNA linear EST 26-MAY-2004  
4129335 BARC 8BOV Bos taurus cDNA clone 8BOV\_50H03 5', mRNA  
sequence.  
CN794193  
CN794193.1 GI:47690173  
EST.  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 571)  
Baumann,R.G.; Baldwin,R.L.; Sonstegard,T.S.; Van Tassell,C.P. and  
Matukumalli,L.K.  
Construction and Analysis of a cDNA Library Generated From  
Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
Unpublished (2004)  
Contact: Richard G. Baumann  
Bovine Functional Genomics Lab  
ANRI  
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA  
Tel: 3015048604  
Fax: 3015048744  
Email: rbaumann@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.00925 using options -trim\_alt '' -trim\_fasta. Vector identified  
by cross\_match using options -minmatch 12 -minscore 18  
Plate: 50 row: H column: 03  
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High quality sequence stop: 571.  
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neonatal intestinal 4/5 Lactating, Proximal Duodenum,  
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal  
Duodenum, Jejunum, Distal Ileum"  
ORIGIN  
Query Match 14.1%; Score 286.4; DB 7; Length 571;  
Best Local Similarity 89.5%; Pred. No. 8.7e-60;  
Matches 308; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1670 CCATGAGCAACAACCTTGGTAAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAG 1729  
DB 1 CCCTAAGCAACAACCTTGGTAAACCCCTCGAAAAACGGGAAACAGCTGGCCGTGAAAAAGACAAG 60



QY 1730 GACTCTATTATATGCCCCAAGTCACCTTCTGTTCCTCCATCGGGAAGCTTCGAGTCAAG 1789  
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Db 61 GATTCTATACATCTACACCCCAAGTCACCTTCTGTTCCTCCATCGGGAACCTTTGAGTCAAG 120  
1790 CTCCATTATAGCCAGCCTCTGCTCTAAAGTCCCGGCTAGATTTCGAGAGAATCTTACTCA 1849  
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Db 121 CTCCATTATAGCCAGCCTCTGCTGAAGTCCCCAAGTGGATCAGAGAGAATCTTACTGA 180  
1850 GAGCTGCAAAATACCCACAGTTTCGCCCAAACCTTCGCGGGCAACATCCATTACATTGGGAG 1909  
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Db 181 GAGCTGCAAAACACCCACAGTTCTTCCAAACCATGCGGGGAGCAATCCATTACATTAGGAG 240  
1910 GAGTATTGTAATTGCAACCAAGTGCTTCGGTGTTCGCTTGTGCAATGTGACTGATCCAAAGCAAG 1969  
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Db 241 GAGTCTTTGAATTGCAATCGGTGCTTCACATCATTTGGCTTACTCAAACTC 344  
1970 TGAGCCATGGCACTGGCTTCACGCTCCTTTGGCTTACTCAAACTC 2013  
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Db 301 TGAGCCACGGGACGGGCTTCACATCATTTGGCTTACTCAAACTC 344

RESULT 7  
CN786611  
LOCUS  
DEFINITION CN786611 628 bp mRNA linear EST 26-MAY-2004  
4120632 BARC 8BOV Bos taurus cDNA clone 8BOV\_29K22 5', mRNA  
sequence.  
ACCESSION CN786611  
VERSION CN786611.1 GI:47682100  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 628)  
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and  
Matukumalli,L.K.  
TITLE Construction and Analysis of a cDNA Library Generated From  
Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Richard G. Baumann  
Bovine Functional Genomics Lab  
ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA  
Tel: 3015048604  
Fax: 3015048744  
Email: rbaumann@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt ',' -trim fasta. Vector identified  
by cross\_match using options -minmatch 12 -minscore 18  
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High quality sequence stop: 628.  
Location/Qualifiers

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Not1; Site 2: EcoRI; Normalized cow cDNA intestinal  
library in pCMVSPORT6.1, constructed from equimolar mRNA  
pools derived from 5 sources, 4 lactating intestinal, 1  
neonatal intestinal 4/5 Lactating, Proximal Duodenum,  
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal  
Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 11.8%; Score 240; DB 7; Length 628;  
Best Local Similarity 89.7%; Pred. No. 2.8e-48;  
Matches 280; Conservative 0; Mismatches 30; Indels 2; Gaps 2;  
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11 GGGAAACAGCTGGCCGTGAAAAGAC-AGGATTCTATTACATCTACACCCAAGTCACCTTC 69  
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QY 1822 CCCGGTAGATTCGAGAGAACTTTACTCAGAGCTGCAATAACCCACAGTTCGCCCAAACCT 1881  
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QY 1882 TCGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTG 1941  
189 TCGGGGCAGCAATCCATTCACTTAGGAGGAGTCTTTGAATTGCAATCGGGTGTTCGGTG 248  
QY 1942 TTTGTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCTTTGGC 2001  
249 TTTGTCAATGTGACTGATCCAAAGTCAAGTGAGCCACGGGACGGGCTTCACATCATTTGGC 308  
QY 2002 TTAACCAAACTC 2013  
Db 309 TTAACCAAACTC 320

RESULT 8  
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LOCUS  
DEFINITION CD640741 702 bp mRNA linear EST 17-JUN-2003  
AGENCOURT\_14542170 NIH\_MGC\_191 Homo sapiens cDNA clone  
IMAGE:30414715 5', mRNA sequence.  
ACCESSION CD640741  
VERSION CD640741.1 GI:31808911  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 702)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDCM211 row: 1 column: 20  
High quality sequence stop: 571.  
Location/Qualifiers

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/clone\_lib="NIH\_MGC\_191"  
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Site 2: SfiI (ggccgctcgcc); Library is oligo-dT primed  
and directionally cloned. PBMC - Peripheral Blood  
Mononuclear Cells. RNA was pooled from 3/6hour stimulation

with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	10.9%;	Score	221.4;	DB 6;	Length	702;
Best Local Similarity	88.4%;	Pred. No.	1.2e-43;			
Matches	252;	Conservative	0;	Mismatches	31;	Indels 2; Gaps 1;
QY	1522	ACAGTGCAAGAGAAAAACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGAT	1581			
Db	362	ATAATGTTAAACAAGAGAGACGAAGAAACACAGCTTTGAAATGCAAAAAGGTGAT	421			
QY	1582	CAGAATCCTCAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTG	1641			
Db	422	CAGAATCCTCAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTG	481			
QY	1642	TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAT	1701			
Db	482	TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAT	541			
QY	1702	GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC	1761			
Db	542	GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTT	601			
QY	1762	TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGC	1806			
Db	602	CTGTCCATCGGGAAGCTTTCGAGTCA--GCTCATTTTATAGCCAGC	644			

RESULT 9

CD642064	CD642064	690 bp	mRNA	linear	EST 17-JUN-2003
LOCUS	AGENCOURT 14538852 NIH MGC_191 Homo sapiens cDNA clone				
DEFINITION	IMAGE:30418744 5', mRNA sequence.				
ACCESSION	CD642064				
VERSION	CD642064.1 GI:31811566				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 690)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDCM222 row: d column: 17 High quality sequence stop: 536.				

FEATURES

source	1. .690
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:30418744"
	/tissue_type="Pooled"

/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	10.7%;	Score	217.2;	DB 6;	Length	690;
Best Local Similarity	92.3%;	Pred. No.	1.3e-42;			
Matches	228;	Conservative	0;	Mismatches	19;	Indels 0; Gaps 0;
QY	1522	ACAGTGCAAGAGAAAAAGACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGAT	1581			
Db	367	ATAATGTTAAACAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAAGGTGAT	426			
QY	1582	CAGAATCCTCAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTG	1641			
Db	427	CAGAATCCTCAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTG	486			
QY	1642	TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAT	1701			
Db	487	TTACAGTGGGCTGANAAAGGATACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAT	546			
QY	1702	GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTC	1761			
Db	547	GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAGTCACCTTC	606			
QY	1762	TGTTCCA 1768				
Db	607	TGTTCCA 613				

RESULT 10

CD520208	CD520208	796 bp	mRNA	linear	EST 06-JUN-2003
LOCUS	AGENCOURT 14355767 NIH MGC_191 Homo sapiens cDNA clone				
DEFINITION	IMAGE:30412573 5', mRNA sequence.				
ACCESSION	CD520208				
VERSION	CD520208.1 GI:31451926				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 796)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDCM206 row: c column: 14 High quality sequence stop: 541.				

FEATURES

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/tissue_type="Pooled"
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/clone_lib="NIH_MGC_191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGGCATATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match      10.4%; Score 211; DB 6; Length 796;
Best Local Similarity 91.4%; Pred. No. 4.5e-41;
Matches 234; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 1522 ACAGTCAAAGAGAAAAAAGACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGAT 1581
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 ATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGAT 418

QY 1582 CAGAAATCCTCAAAATTGCGGCACATGTTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTG 1641
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 419 CAGAAATCCTCAAAATTGCGGCACATGTTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTG 478

QY 1642 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACCTGGAAAAAT 1701
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 TTACAGTNGCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACCTGGAAAAAT 538

QY 1702 GGGAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATATGCCCCAAGTCA-CCTT 1760
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 539 GGGAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATATGCCCCAAGTCA-CCTT 598

QY 1761 CTGTTCCAAATCGGGAA 1776
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Db 599 CTGTTCCAAATCGGGAA 614

RESULT 11
BH886550/c
LOCUS
DEFINITION
  BH886550
  BH886550.1 GI:22130945
  GSS.
  Leishmania major
  Leishmania major
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Leishmania.
  1 (bases 1 to 527)
  Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E.,
  Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E.,
  Stuart,K. and Ragland,M.
  Leishmania major Friedlin BAC End Sequences
  Unpublished (2002)
  Other_GSSs: LB00861a.d.T7.1
  Contact: Myler PJ
  Seattle Biomedical Research Institute
  4 Nickerson Street, Seatttle, WA 98109-1651, USA
  Tel: 206 284-8846
  Fax: 206 284-0313
  Email: mylerpj@sbri.org

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cross match v0.990329.
Plate_33 row: N column: 5
Seq primer: GTAATACGACTCACTATAGGG.
FEATURES
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    Best Local Similarity 91.3%;   Pred. No. 1.2e-15;
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QY      1888 CAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTC 1947
Db      847  CAGCAATCCATTCACTTAGGAGGAGTCTTTGAATTGCAATCGGCGTTCGCGTGTGTC 788

QY      1948 AATGTGACTGATCCAAGCCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTC 2007
Db      787 AATGTGACTGATCCAAGTCAAGTCAGTGAGCCACGGGACGGGCTTCACATCATTTGGCTTACTC 728

QY      2008 AAATCT 2013
Db      727 AAATCT 722

RESULT 13
CK834247
LOCUS      CK834247.1   GI:45064536          740 bp   mRNA   linear   EST 04-MAR-2004
DEFINITION 4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA
sequence.
ACCESSION  CK834247
VERSION    CK834247.1
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 740)
AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
TITLE     Intestinal Muscle and Analysis of a cDNA Library Generated From
            Construction and Epithelial Tissues of Holstein Cattle
JOURNAL   Unpublished (2004)
COMMENT   Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim alt ',' -trim fasta. Vector identified
            by cross match using options -minmatch 12 -minscore 12
            Plate: 2 row: M column: 16
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/sex="Female"
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/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
ORIGIN
    Query Match          5.2%;   Score 105.2;   DB 7;   Length 740;
    Best Local Similarity 79.1%;   Pred. No. 7.3e-15;
    Matches 125;   Conservative 0;   Mismatches 33;   Indels 0;   Gaps 0;

QY      1522 ACAGTGCAAAAGAGAAAAAGACCGGATCCAGAAAACAGCTTTGAAATGCCAAAAGGTGAT 1581
Db      583 ATAATGCAAAACAAAGAAGTAAAGAGAAAGAAAAAACTTTGAAATGCACAAAGGTGAT 642

QY      1582 CAGAATCCTCAAAATTGCGGCACATGTCTAATAGTGAGGCCAGCAGTAGTAAAAACATCTGTG 1641
Db      643 CAGGAGCCTCAGATACGCGGCACATGTCTATCATGAGGCCAGTAGTAAACACACCTCTGTT 702

QY      1642 TTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAA 1679
Db      703 CTCCAGTGGGCCCCCAAGGATACTACACCCCTAAGCAA 740

RESULT 14
BF599437
LOCUS      BF599437          492 bp   mRNA   linear   EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BF599437
VERSION    BF599437.1   GI:11695919
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 492)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
PUBMED    11282978
COMMENT   Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross match with the -minscore 18
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            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 2483.19 Seconds  
(without alignments)  
16453.933 Million cell updates/sec

Title: US-09-687-864A-17  
Perfect score: 864  
Sequence: 1 aagcttgccgccatgctgta.....aactcgagtataatctaga 864

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues 9053458  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642.8	74.4	786	6 I87864	I87864 Sequence 3
2	642.8	74.4	786	6 BD064000	BD064000 Novel exp
3	642.8	74.4	786	6 BD064003	BD064003 Novel exp
4	642.8	74.4	786	6 BD064005	BD064005 Novel exp
5	642.8	74.4	786	6 BD064006	BD064006 Novel exp
6	642.8	74.4	840	6 AR044779	AR044779 Sequence
7	642.8	74.4	840	6 AR076926	AR076926 Sequence
8	642.8	74.4	840	6 AR078316	AR078316 Sequence
9	642.8	74.4	840	6 AR085419	AR085419 Sequence
10	642.8	74.4	840	6 AR103375	AR103375 Sequence
11	642.8	74.4	840	6 AR106246	AR106246 Sequence
12	642.8	74.4	840	6 AR169232	AR169232 Sequence
13	642.8	74.4	840	6 AR171647	AR171647 Sequence
14	642.8	74.4	840	6 BD190674	BD190674 Method of
15	642.8	74.4	840	6 I23893	I23893 Sequence 1
16	642.8	74.4	840	6 I27345	I27345 Sequence 7
17	642.8	74.4	840	6 I67828	I67828 Sequence 1
18	642.8	74.4	840	6 AR216259	AR216259 Sequence
19	642.8	74.4	840	6 AR267621	AR267621 Sequence

20	642.8	74.4	870	9 BC074950	BC074950 Homo sapi
21	642.8	74.4	879	6 AR254616	AR254616 Sequence
22	642.8	74.4	879	6 AX090039	AX090039 Sequence
23	642.8	74.4	879	9 HSGP39MR	Z15017 H.sapiens m
24	642.8	74.4	1803	6 AR350226	AR350226 Sequence
25	642.8	74.4	1803	9 HSCD40	X67878 H.sapiens m
26	642.8	74.4	1816	6 BD187611	BD187611 Screening
27	642.8	74.4	1816	6 BD270930	BD270930 Use of CD
28	642.8	74.4	1816	6 AR254617	AR254617 Sequence
29	642.8	74.4	1816	9 HUMCD40L	L07414 Human CD40-
30	642.8	74.4	1859	9 BC071754	BC071754 Homo sapi
31	641.2	74.2	1798	6 CQ725625	CQ725625 Sequence
32	641.2	74.2	1822	9 HSTRAPA	X68550 H.sapiens T
33	638.4	73.9	1566	6 AX455878	AX455878 Sequence
34	636	73.6	929	6 AR076932	AR076932 Sequence
35	636	73.6	929	6 AR078322	AR078322 Sequence
36	636	73.6	929	6 AR085425	AR085425 Sequence
37	636	73.6	929	6 AR103381	AR103381 Sequence
38	636	73.6	929	6 AR169238	AR169238 Sequence
39	636	73.6	929	6 I87867	I87867 Sequence 10
40	636	73.6	929	6 AR216265	AR216265 Sequence
41	635.2	73.5	1425	6 AR076929	AR076929 Sequence
42	635.2	73.5	1425	6 AR078319	AR078319 Sequence
43	635.2	73.5	1425	6 AR085422	AR085422 Sequence
44	635.2	73.5	1425	6 AR103378	AR103378 Sequence
45	635.2	73.5	1425	6 AR169235	AR169235 Sequence

ALIGNMENTS

RESULT 1

I87864

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .786

/organism="unknown"

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ORIGIN

I87864	I87864	Sequence 3 from patent US 5716805.	786 bp	DNA	linear	PAT 10-AUG-1998
DEFINITION	Sequence 3 from patent US 5716805.					
ACCESSION	I87864					
VERSION	I87864.1	GI:3407804				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 786)					
AUTHORS	Srinivasan,S. and Spriggs,M.K.					
TITLE	Methods of preparing soluble, oligomeric proteins					
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;					
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Best Local Similarity	99.7%;	Pred. No. 5.1e-157;		
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Qy	204	TCCAAGAAGTTGGACAAGATAGAAGATGAAGGAATCTTTCATGAAGATTTGTATTTCAT	263	
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Qy	264	GAACACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323	
Db	198	GAACACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	257	
Qy	324	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGCATATAATGTTAAACAAAGAGAGACGAA	383	
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Qy	384	GAAGAAAAACAGTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT	443	
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Db	378	CATAAGTGAGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	437
QY	504	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA	563
Db	438	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA	497
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAAGCTTCGAGTCA	623
Db	498	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAAGCTTCGAGTCA	557
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCTTTACT	683
Db	558	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCTTTACT	617
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAACAATCCATTCACTTGGG	743
Db	618	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAACAATCCATTCACTTGGG	677
QY	744	AGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	737
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	849
Db	738	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	783
RESULT 2			
BD064000			
LOCUS			
DEFINITION		Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.	
ACCESSION		BD064000	
VERSION		BD064000.1 GI:22609603	
KEYWORDS		JP 2001505782-A/1.	
SOURCE		synthetic construct	
ORGANISM		synthetic construct	
REFERENCE		artificial sequences.	
AUTHORS		1 (bases 1 to 786)	
TITLE		Kipps,T.J., Sharma,S. and Cantwell,M.	
JOURNAL		Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease	
COMMENT		Patent: JP 2001505782-A 1 08-MAY-2001; UNIVERSITY OF CALIFORNIA	
FEATURES		source	
ORIGIN		786 bp DNA linear PAT 27-AUG-2002	
Query Match		74.4%; Score 642.8; DB 6; Length 786;	
Best Local Similarity		99.7%; Pred. No. 5.1e-157;	
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QY	204	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	263
Db	138	TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	197
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Db	198	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	257
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QY	384	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGCGGCACATGT	443
Db	318	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGCGGCACATGT	377
QY	444	CATAAGTGAGGCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	503
Db	378	CATAAGTGAGGCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	437
QY	504	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA	563
Db	438	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA	497
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAAGCTTCGAGTCA	623
Db	498	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAAGCTTCGAGTCA	557
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCTTTACT	683
Db	558	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCTTTACT	617
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAACAATCCATTCACTTGGG	743
Db	618	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAACAATCCATTCACTTGGG	677
QY	744	AGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	737
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	849
Db	738	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	783
RESULT 3			
BD064003			
LOCUS			
DEFINITION		Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.	
ACCESSION		BD064003	
VERSION		BD064003.1 GI:22609606	
KEYWORDS		JP 2001505782-A/4.	
SOURCE		synthetic construct	
ORGANISM		synthetic construct	
REFERENCE		artificial sequences.	
AUTHORS		1 (bases 1 to 786)	
TITLE		Kipps,T.J., Sharma,S. and Cantwell,M.	
JOURNAL		Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease	
COMMENT		Patent: JP 2001505782-A 4 08-MAY-2001; UNIVERSITY OF CALIFORNIA	
FEATURES		source	
ORIGIN		786 bp DNA linear PAT 27-AUG-2002	
Query Match		74.4%; Score 642.8; DB 6; Length 786;	
Best Local Similarity		99.7%; Pred. No. 5.1e-157;	
Matches 644; Conservative		0; Mismatches 2; Indels 0; Gaps 0;	
QY	204	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	263
Db	138	TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	197
QY	264	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323





VERSION BD064006.1 GI:22609609  
KEYWORDS JP 2001505782-A/7.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 786)  
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.  
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease  
JOURNAL Patent: JP 2001505782-A 7 08-MAY-2001;  
UNIVERSITY OF CALIFORNIA  
COMMENT PN JP 2001505782-A/7  
PD 08-MAY-2001  
PF 08-DEC-1997 JP 1998526956  
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI  
THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL  
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/705,  
PC C12N15/86,  
PC A61K48/00,A61K38/17,A61K35/12  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES source  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 74.4%; Score 642.8; DB 6; Length 786;  
Best Local Similarity 99.7%; Pred. No. 5.1e-157;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 138 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
Db 198 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 257  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383  
Db 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTGCGGCACATGT 443  
Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTGCGGCACATGT 377  
QY 444 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 378 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 437  
QY 504 CACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 563  
Db 438 CACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 497  
QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 623  
Db 498 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 557  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 683  
Db 558 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 617  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGAACAAATCCATTCACTTGGG 743  
Db 618 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGAACAAATCCATTCACTTGGG 677  
QY 744 AGGAGTATTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803  
Db 678 AGGAGTATTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 737

QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 849  
Db 738 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 783  
RESULT 6  
LOCUS AR044779 AR044779 840 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5817516.  
ACCESSION AR044779  
VERSION AR044779.1 GI:5966244  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Kehry,M. and Castle,B.  
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand  
JOURNAL Patent: US 5817516-A 3 06-OCT-1998;  
FEATURES Location/Qualifiers  
source  
1..840  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 74.4%; Score 642.8; DB 6; Length 840;  
Best Local Similarity 99.7%; Pred. No. 5.1e-157;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 159 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 218  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
Db 219 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383  
Db 279 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 338  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTGCGGCACATGT 443  
Db 339 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTGCGGCACATGT 398  
QY 444 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 399 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 458  
QY 504 CACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 563  
Db 459 CACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 518  
QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 623  
Db 519 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 578  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 683  
Db 579 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 638  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGAACAAATCCATTCACTTGGG 743  
Db 639 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGAACAAATCCATTCACTTGGG 698  
QY 744 AGGAGTATTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803  
Db 699 AGGAGTATTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 758  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 849

Db 759 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 804

RESULT 7  
AR076926  
LOCUS AR076926 840 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 11 from patent US 5961974.  
ACCESSION AR076926  
VERSION AR076926.1 GI:10003672  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.  
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same  
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..840  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 74.4%; Score 642.8; DB 6; Length 840;  
Best Local Similarity 99.7%; Pred. No. 5.1e-157;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGGAAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGGAAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323  
Db 243 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443  
Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 423 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAAACAGCTGACCCGTTAAAAAGACA 563  
Db 483 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAAACAGCTGACCCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 623  
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 683  
Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 662

QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 743  
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 803  
Db 723 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 782

QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 849  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 828

RESULT 8  
AR078316  
LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 11 from patent US 5962406.  
ACCESSION AR078316  
VERSION AR078316.1 GI:10005062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S., Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same  
JOURNAL Patent: US 5962406-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..840  
/organism="unknown"  
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ORIGIN  
Query Match 74.4%; Score 642.8; DB 6; Length 840;  
Best Local Similarity 99.7%; Pred. No. 5.1e-157;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGGAAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGGAAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323  
Db 243 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443  
Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAAACAGCTGACCCGTTAAAAAGACA 563  
Db 483 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAAACAGCTGACCCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 623  
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 683  
Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 662

QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 743  
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 803  
Db 723 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 782

QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 849  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 828

RESULT 9  
AR085419

LOCUS	AR085419	840 bp	DNA	linear	PAT 01-SEP-2000
DEFINITION	Sequence 11 from patent US 5981724.				
ACCESSION	AR085419				
VERSION	AR085419.1	GI:10012188			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 840)				
AUTHORS	Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S., Gibson,M.G., Morris,A.E. and McGrew,J.T.				
TITLE	DNA encoding CD40 ligand, a cytokine that binds CD40				
JOURNAL	Patent: US 5981724-A 11 09-NOV-1999;				
FEATURES	Location/Qualifiers				
source	1..840				
	/organism="unknown"				
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ORIGIN					
	Query Match	74.4%;	Score 642.8;	DB 6;	Length 840;
	Best Local Similarity	99.7%;	Pred. No. 5.1e-157;		
	Matches 644;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	204	TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	263		
Db	183	TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	242		
QY	264	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA	323		
Db	243	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA	302		
QY	324	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383		
Db	303	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	362		
QY	384	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT	443		
Db	363	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT	422		
QY	444	CATAAGTGAGGCCAGCAGTAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503		
Db	423	CATAAGTGAGGCCAGCAGTAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482		
QY	504	CACCATGAGCAACAACTTGGTAAACCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA	563		
Db	483	CACCATGAGCAACAACTTGGTAAACCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA	542		
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATTCGGGAAGCTTCGAGTCA	623		
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATTCGGGAAGCTTCGAGTCA	602		
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	683		
Db	603	AGCTCCATTATAGCCAGCCTCTGCCTAAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	662		
QY	684	CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	743		
Db	663	CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	722		
QY	744	AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA	803		
Db	723	AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA	782		
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC	849		
Db	783	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC	828		
RESULT 10					
AR103375					
LOCUS	AR103375	840 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 11 from patent US 6087329.				
ACCESSION	AR103375				

VERSION		AR103375.1		GI:12814963	
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unknown.			
REFERENCE		Unclassified.			
AUTHORS		1 (bases 1 to 840)			
TITLE		Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.			
JOURNAL		CD40 ligand polypeptide			
FEATURES		Patent: US 6087329-A 11 11-JUL-2000;			
source		Location/Qualifiers			
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		/organism="unknown"			
		/mol_type="unassigned DNA"			
ORIGIN					
Query Match		74.4%;		Score 642.8; DB 6; Length 840;	
Best Local Similarity		99.7%;		Pred. No. 5.1e-157;	
Matches 644;		Conservative 0;		Mismatches 2; Indels 0; Gaps 0;	
QY	204	TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	263		
Db	183	TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	242		
QY	264	GAAACCGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323		
Db	243	GAAACCGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	302		
QY	324	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	383		
Db	303	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	362		
QY	384	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCACATGT	443		
Db	363	GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCACATGT	422		
QY	444	CATAAGTGAGGCCAGCAGTAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503		
Db	423	CATAAGTGAGGCCAGCAGTAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482		
QY	504	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563		
Db	483	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	542		
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	623		
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	602		
QY	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT	683		
Db	603	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT	662		
QY	684	CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGCAACAATCCATTCACCTTGGG	743		
Db	663	CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGGCAACAATCCATTCACCTTGGG	722		
QY	744	AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA	803		
Db	723	AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA	782		
QY	804	AGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	849		
Db	783	AGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	828		
RESULT 11					
LOCUS		AR106246			
DEFINITION		Sequence 7 from patent US 6106832.		linear PAT 14-FEB-2001	
ACCESSION		AR106246			
VERSION		AR106246.1		GI:12820776	
KEYWORDS		Unknown.			
SOURCE		Unknown.			



REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.  
TITLE Treatment of individuals exhibiting defective CD40L  
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..840  
/organism="unknown"  
/mol\_type="unassigned DNA"  
  
ORIGIN  
Query Match 74.4%; Score 642.8; DB 6; Length 840;  
Best Local Similarity 99.7%; Pred. No. 5.1e-157;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 204 TCCAAGAAGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 263  
|||  
Db 183 TCATAGAAGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 242  
  
Qy 264 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
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Db 243 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
  
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
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ACCESSION AR169232  
VERSION AR169232.1 GI:17907047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.

TITLE Method of augmenting a vaccine response by administering CD40 ligand  
JOURNAL Patent: US 6290972-A 11 18-SEP-2001;  
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Db 243 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
  
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Qy 804 AGTGAGCCATGGCAGCTGGCTTCACGTCTTGGCTTACTCAAACTC 849  
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LOCUS AR171647 840 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 3 from patent US 6297052.  
ACCESSION AR171647  
VERSION AR171647.1 GI:17910597  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Kehry,M. and Castle,B.  
TITLE B cell culture system comprising high density membrane bound CD40 ligand  
JOURNAL Patent: US 6297052-A 3 02-OCT-2001;



ORGANISM	Unknown.									
REFERENCE	Unclassified.									
AUTHORS	1 (bases 1 to 840)									
TITLE	Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.									
JOURNAL	Soluble and its use in B cell stimulation									
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QY	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	623							
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QY	684	CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTCGGGCAACAATCCATTCACTTGGG	743							
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	810.4	93.8	906	4	Aaf82932 HIV-1 gp1
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4	665	77.0	2252	4	Aaf82928 HIV-1 gp1
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37	639.8	74.1	840	2	AAT58122	Aat58122 Human CD4
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ALIGNMENTS

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AC AAF82933;  
XX

DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX

DE HIV-1 gp120 V3 loop-CD154 long form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
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OS Human immunodeficiency virus 1.  
OS Homo sapiens.

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WO200126608-A2.

19-APR-2001.

13-OCT-2000; 2000WO-US028414.

14-OCT-1999; 99US-0159690P.

(LEDB/) LEDBETTER J A.





CC The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human  
CC CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
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DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
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OS Homo sapiens.  
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PF 13-OCT-2000; 2000WO-US028414.  
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PR 14-OCT-1999; 99US-0159690P.  
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PA (HAYD/) HAYDEN-LEDBETTER M S.  
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PI Ledbetter JA, Hayden-Ledbetter MS;  
XX  
DR WPI; 2001-281790/29.  
DR P-PSDB; AAB62334.  
XX  
PT DNA vaccine for improving antigen-specific humoral and cellular immune  
PT responses, comprising one or more antigens linked to a domain that binds  
PT at least one receptor.  
XX  
PS Example 1; Fig 3A; 55pp; English.  
XX  
CC The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC long form extracellular domain fusion protein linked by a ProAspPro  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
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Query Match      78.3%; Score 676.2; DB 4; Length 2209;
Best Local Similarity 94.2%; Pred. No. 2.6e-181;
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QY 780 TGTCAATGTGACTGATCCAAGCCAAAGTGAGCCATGGCAGCTTCAGTCCTTTGGCTT 839
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Db 2124 TGTCAATGTGACTGATCCAAGCCAAAGTGAGCCATGGCAGCTTCAGTCCTTTGGCTT 2183

QY 840 ACTCAAACTCGAGTGATAATCTAGA 864
    |||||
Db 2184 ACTCAAACTCGAGTGATAATCTAGA 2208
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```
RESULT 4
AAF82928
ID AAF82928 standard; cDNA; 2252 BP.
XX AC AAF82928;
XX AC AAF82928;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
```

```
XX OS Human immunodeficiency virus 1.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 13..2252
FT /*tag= a
FT sig_peptide 13..72
FT /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /*tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1593
FT /*tag= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 1594..2252
FT /*tag= e
FT /note= "human CD154 long form extracellular domain coding
    sequence"
PN WO200126608-A2.
XX 19-APR-2001.
XX 13-OCT-2000; 2000WO-US028414.
XX 14-OCT-1999; 99US-0159690P.
PA (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
PI Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
DR P-PSDB; AAB62333.
XX DNA vaccine for improving antigen-specific humoral and cellular immune
    responses, comprising one or more antigens linked to a domain that binds
    at least one receptor.
XX Example 1; Fig 3A; 55pp; English.
XX The invention provides a vaccine comprising one or more antigens linked
    to a domain that binds at least one receptor to improve the antigen-
    specific humoral and cellular immune response. The DNA vaccines induce
    strong antigen-specific humoral and cellular immune responses. The
    vaccine can be use against acquired immunodeficiency syndrome (AIDS). The
    present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
    long form extracellular domain fusion protein linked by (Gly4Ser)3
    linker. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;
SQ Query Match      77.0%; Score 665; DB 4; Length 2252;
    Best Local Similarity 100.0%; Pred. No. 3.9e-178;
    Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 CGGATCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGAT 259
    |||||
Db 1586 CGGATCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGAT 1645

QY 260 TCATGAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACGTG 319
    |||||
Db 1646 TCATGAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACGTG 1705

QY 320 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 379
    |||||
Db 1706 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 1765

QY 380 CGAAGAAAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 439
    |||||
Db 1766 CGAAGAAAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 1825
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QY 560 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 619  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1225  
  
QY 620 GTCAAGCTCCATTTATAGCAGCCTCTGCGCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 679  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1226 GTCAAGCTCCATTTATAGCAGCCTCTGCGCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1285  
  
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGGGGCAACAATCCATTCACT 739  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGGGGCAACAATCCATTCACT 1345  
  
QY 740 TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTGTCAATGTGACTGATCCAA 799  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1346 TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTGTCAATGTGACTGATCCAA 1405  
  
QY 800 GCCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGGTTACTCAAACTCGAGTGATAAT 859  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1406 GCCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGGTTACTCAAACTCGAGTGATAAT 1465  
  
QY 860 CTAGA 864  
Db |||||  
1466 CTAGA 1470

RESULT 6  
ADD25460  
ID ADD25460 standard; DNA; 1470 BP.  
XX  
AC ADD25460;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Binding domain-immunoglobulin fusion protein-associated DNA #11.  
XX  
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX  
OS Unidentified.  
XX  
PN US2003118592-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 25-JUL-2002; 2002US-00207655.  
XX  
PR 17-JAN-2001; 2001US-0367358P.  
PR 17-JAN-2002; 2002US-00053530.  
PR 03-JUN-2002; 2002US-0385691P.  
XX  
PA (GENE-) GENERAFT INC.  
XX  
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
XX  
DR WPI; 2003-801317/75.  
XX  
PT New binding domain-immunoglobulin fusion protein, useful for treating a  
PT subject having or suspected of having a malignant condition or a B-cell  
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX  
PS Disclosure; SEQ ID NO 21; 157pp; English.  
XX  
CC Unidentified  
XX  
SQ Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;  
Query Match 76.8%; Score 663.4; DB 10; Length 1470;

Best Local Similarity 99.8%; Pred. No. 9.4e-178;  
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 200 CGGATCCAAGAAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTAT 259  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
806 CTGATCCAAGAAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTAT 865  
  
QY 260 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTG 319  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
866 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTG 925  
  
QY 320 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGA 379  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
926 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGA 985  
  
QY 380 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGTGATCAGAATCCTCAAAATTCGCGCAC 439  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
986 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGTGATCAGAATCCTCAAAATTCGCGCAC 1045  
  
QY 440 ATGTCATAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGGGCTGAAAAAGGAT 499  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1046 ATGTCATAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGGGCTGAAAAAGGAT 1105  
  
QY 500 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 559  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1106 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 1165  
  
QY 560 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAAATCGGGAAGCTTCGA 619  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAAATCGGGAAGCTTCGA 1225  
  
QY 620 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 679  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1226 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1285  
  
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGGGCAACAATCCATTCACT 739  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGGGCAACAATCCATTCACT 1345  
  
QY 740 TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTGTCAATGTGACTGATCCAA 799  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1346 TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTGTCAATGTGACTGATCCAA 1405  
  
QY 800 GCCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGGTTACTCAAACTCGAGTGATAAT 859  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1406 GCCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGGTTACTCAAACTCGAGTGATAAT 1465  
  
QY 860 CTAGA 864  
Db |||||  
1466 CTAGA 1470

RESULT 7  
ADD25588  
ID ADD25588 standard; DNA; 1470 BP.  
XX  
AC ADD25588;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Binding domain-immunoglobulin fusion protein-associated DNA #78.  
XX  
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX  
OS Unidentified.  
XX







```
Query Match      74.4%; Score 642.8; DB 2; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAAT 263
Db 138 TCATAGAAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAAT 197

QY 264 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323
Db 198 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 257

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317

QY 384 GAAAAAGATACAGAGATGCAACACAGGAGAAAGTGAAGGAATCCTCAAAATTCGCGGCACATGT 443
Db 318 GAAAAAGATACAGAGATGCAACACAGGAGAAAGTGAAGGAATCCTCAAAATTCGCGGCACATGT 377

QY 444 CATAAGTGAGGCCAGCAGTAAAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db 378 CATAAGTGAGGCCAGCAGTAAAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 437

QY 504 CACCATGAGCAACAACTTGTGAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTGTGAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497

QY 564 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557

QY 624 AGCTCCATTATAGCCAGCTCTGCCCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 683
Db 558 AGCTCCATTATAGCCAGCTCTGCCCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 617

QY 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAACAATCCATTCCTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAACAATCCATTCCTTGGG 677

QY 744 AGGAGTATTGAAATTGCAACAGGCTTCGGTGTTCGATGCTGCTGCTGCTGCTGCTGCTGCT 803
Db 678 AGGAGTATTGAAATTGCAACAGGCTTCGGTGTTCGATGCTGCTGCTGCTGCTGCTGCTGCT 737

QY 804 AGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 849
Db 738 AGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 783

RESULT 10
AAV39002
ID AAV39002 standard; DNA; 786 BP.
XX
AC AAV39002;
XX
XX 17-OCT-2003 (revised)
DT 23-SEP-1998 (first entry)
XX
DE Exemplary CD40 ligand gene used in the course of the invention.
XX
KW CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO9826061-A2.
XX
PD 18-JUN-1998.
XX
PF 08-DEC-1997; 97WO-US022740.
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XX 09-DEC-1996; 96US-0032145P.
PR 01-DEC-1997; 97US-00982272.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Kipps TJ, Sharma S, Cantwell M;
XX
DR WPI; 1998-348521/30.
XX
PT Vectors containing accessory molecule ligand genes - used for altering
PT immunoreactivity of cells, particularly for treatment of neoplasia or
PT autoimmune disorders, e.g. rheumatoid arthritis.
XX
PS Disclosure; Page 106; 167pp; English.
XX
CC The present sequence represents an exemplary CD40 ligand gene, comprising
CC nucleotides encoding the extracellular domains (Domains III and IV) and
CC transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998)
CC operatively linked to nucleotides encoding the cytoplasmic domain (Domain
CC I) of the murine CD40 ligand gene (AAV38997). The sequence is used to
CC exemplify the method of the invention. The specification describes a
CC method for altering the immunoreactivity of human cells which comprises
CC introducing a gene encoding an accessory molecule ligand (AML) into the
CC cells so that the AML is expressed on the surface of the cells. Vectors
CC containing the AML genes can be used in gene therapy for treating
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can
CC also be used for vaccination to produce immunity against a virus cell,
CC bacteria, protein, fungus or neoplasia. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 786 BP; 250 A; 166 C; 171 G; 199 T; 0 U; 0 Other;

Query Match      74.4%; Score 642.8; DB 2; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAAT 263
Db 138 TCATAGAAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAAT 197

QY 264 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323
Db 198 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 257

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317

QY 384 GAAAAAGATACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTCGCGGCACATGT 443
Db 318 GAAAAAGATACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTCGCGGCACATGT 377

QY 444 CATAAGTGAGGCCAGCAGTAAAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db 378 CATAAGTGAGGCCAGCAGTAAAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 437

QY 504 CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497

QY 564 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557

QY 624 AGCTCCATTATAGCCAGCTCTGCCCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 683
Db 558 AGCTCCATTATAGCCAGCTCTGCCCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT 617

QY 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAACAATCCATTCCTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAACAATCCATTCCTTGGG 677

QY 744 AGGAGTATTGAAATTGCAACAGGCTTCGGTGTTCGATGCTGCTGCTGCTGCTGCTGCTGCT 803
Db 678 AGGAGTATTGAAATTGCAACAGGCTTCGGTGTTCGATGCTGCTGCTGCTGCTGCTGCTGCT 737

QY 804 AGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 849
Db 738 AGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 783

RESULT 10
AAV39002
ID AAV39002 standard; DNA; 786 BP.
XX
AC AAV39002;
XX
XX 17-OCT-2003 (revised)
DT 23-SEP-1998 (first entry)
XX
DE Exemplary CD40 ligand gene used in the course of the invention.
XX
KW CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO9826061-A2.
XX
PD 18-JUN-1998.
XX
PF 08-DEC-1997; 97WO-US022740.
```

QY	744	AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCGTTGTCATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCGTTGTCATGTGACTGATCCAAAGCCA	737
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC	849
Db	738	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC	783
RESULT 11			
AAV39000			
ID	AAV39000 standard; DNA; 786 BP.		
XX	AAV39000;		
XX	17-OCT-2003 (revised)		
DT	23-SEP-1998 (first entry)		
XX	Exemplary CD40 ligand gene used in the course of the invention.		
DE	CD40 ligand; alteration; immunoreactivity; human cell;		
XX	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;		
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.		
KW			
XX			
OS	Mus sp.		
OS	Homo sapiens.		
OS	Chimeric.		
XX			
PN	WO9826061-A2.		
XX			
PD	18-JUN-1998.		
XX			
PF	08-DEC-1997; 97WO-US022740.		
XX			
PR	09-DEC-1996; 96US-0032145P.		
PR	01-DEC-1997; 97US-00982272.		
XX			
PA	(REGC ) UNIV CALIFORNIA.		
XX			
PI	Kipps TJ, Sharma S, Cantwell M;		
XX			
DR	WPI; 1998-348521/30.		
XX			
PT	Vectors containing accessory molecule ligand genes - used for altering		
PT	immunoreactivity of cells, particularly for treatment of neoplasia or		
PT	autoimmune disorders, e.g. rheumatoid arthritis.		
XX			
PS	Disclosure; Page 105; 167pp; English.		
XX			
CC	The present sequence represents an exemplary CD40 ligand gene, comprising		
CC	nucleotides encoding the extracellular domains (Domains III and IV) of		
CC	human CD40 ligand gene (AAV38998) are operatively linked to nucleotides		
CC	encoding the murine CD40 ligand transmembrane domain (Domain I)		
CC	(AAV38997) which is operatively linked to the human CD40 ligand gene		
CC	cytoplasmic domain (Domain I). The sequence is used to exemplify the		
CC	method of the invention. The specification describes a method for		
CC	altering the immunoreactivity of human cells which comprises introducing		
CC	a gene encoding an accessory molecule ligand (AML) into the cells so that		
CC	the AML is expressed on the surface of the cells. Vectors containing the		
CC	AML genes can be used in gene therapy for treating neoplasia or		
CC	autoimmune disorders such as rheumatoid arthritis. They can also be used		
CC	for vaccination to produce immunity against a virus cell, bacteria,		
CC	protein, fungus or neoplasia. (Updated on 17-OCT-2003 to standardise OS		
CC	field)		
XX			
SQ	Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 U; 0 Other;		
Query Match 74.4%; Score 642.8; DB 2; Length 786;			
Best Local Similarity 99.7%; Pred. No. 5.2e-172;			
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	204	TCCAAGAAGGTTGGACAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263
Db			

Db	138	TCATAGAAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	197
QY	264	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323
Db	198	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	257
QY	324	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383
Db	258	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	317
QY	384	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGCGCACATGT	443
Db	318	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGCGCACATGT	377
QY	444	CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503
Db	378	CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	437
QY	504	CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAACAGCTGACCCGTTAAAAAGACA	563
Db	438	CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAACAGCTGACCCGTTAAAAAGACA	497
QY	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	623
Db	498	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	557
QY	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCTTACT	683
Db	558	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCTTACT	617
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG	743
Db	618	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG	677
QY	744	AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTCATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTCATGTGACTGATCCAAAGCCA	737
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAAC TC 849	
Db	738	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAAC TC 783	

RESULT 12	
AAV38997	
ID	AAV38997 standard; DNA; 786 BP.
XX	
AC	AAV38997;
XX	
DT	23-SEP-1998 (first entry)
XX	
DE	CD40 ligand gene used in the course of the invention.
XX	
KW	CD40 ligand; alteration; immunoreactivity; human cell;
KW	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW	autoimmune disorder; rheumatoid arthritis; vaccine; ss.
XX	
OS	Mus sp.
XX	
PN	WO9826061-A2.
XX	
PD	18-JUN-1998.
XX	
PF	08-DEC-1997; 97WO-US022740.
XX	
PR	09-DEC-1996; 96US-0032145P.
PR	01-DEC-1997; 97US-00982272.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Kipps TJ, Sharma S, Cantwell M;
XX	
DR	WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for altering  
PT immunoreactivity of cells, particularly for treatment of neoplasia or  
PT autoimmune disorders, e.g. rheumatoid arthritis.  
XX  
XX  
PS Disclosure; Page 104; 167pp; English.  
XX  
CC The present sequence represents the CD40 ligand gene. The sequence is  
CC used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells which  
CC comprises introducing a gene encoding an accessory molecule ligand (AML)  
CC into the cells so that the AML is expressed on the surface of the cells.  
CC Vectors containing the AML genes can be used in gene therapy for treating  
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can  
CC also be used for vaccination to produce immunity against a virus cell,  
CC bacteria, protein, fungus or neoplasia  
XX  
SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 U; 0 Other;  
  
Query Match 74.4%; Score 642.8; DB 2; Length 786;  
Best Local Similarity 99.7%; Pred. No. 5.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db |||  
QY 138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197  
Db |||  
QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 323  
Db |||  
QY 198 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 257  
Db |||  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db |||  
QY 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 317  
Db |||  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT 443  
Db |||  
QY 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT 377  
Db |||  
QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503  
Db |||  
QY 378 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 437  
Db |||  
QY 504 CACCATGAGCAACAACCTTGTTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563  
Db |||  
QY 438 CACCATGAGCAACAACCTTGTTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497  
Db |||  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 623  
Db |||  
QY 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 557  
Db |||  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTTTACT 683  
Db |||  
QY 558 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTTTACT 617  
Db |||  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGCGGCAACAATCCATTCACTTGGG 743  
Db |||  
QY 618 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGCGGCAACAATCCATTCACTTGGG 677  
Db |||  
QY 744 AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCCAAGCCA 803  
Db |||  
QY 678 AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCCAAGCCA 737  
Db |||  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849  
Db |||  
QY 738 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 783  
Db |||  
  
RESULT 13  
ID AAV39003 standard; DNA; 786 BP.  
XX  
AC AAV39003;

XX 17-OCT-2003 (revised)  
DT 23-SEP-1998 (first entry)  
XX  
XX Exemplary CD40 ligand gene used in the course of the invention.  
DE  
XX  
XX CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
PN WO9826061-A2.  
XX  
PD 18-JUN-1998.  
XX  
XX 08-DEC-1997; 97WO-US022740.  
PF  
XX 09-DEC-1996; 96US-0032145P.  
PR  
PR 01-DEC-1997; 97US-00982272.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Kipps TJ, Sharma S, Cantwell M;  
PI  
XX WPI; 1998-348521/30.  
DR  
XX Vectors containing accessory molecule ligand genes - used for altering  
PT immunoreactivity of cells, particularly for treatment of neoplasia or  
PT autoimmune disorders, e.g. rheumatoid arthritis.  
XX  
PS Disclosure; Page 107; 167pp; English.  
XX  
CC The present sequence represents an exemplary CD40 ligand gene, comprising  
CC nucleotides encoding the extracellular domains (Domains III and IV) of  
CC the human CD40 ligand gene (AAV38998) operatively linked to nucleotides  
CC encoding the cytoplasmic domain (Domain I) and transmembrane domain  
CC (Domain II) of the murine CD40 ligand gene (AAV38997). The sequence is  
CC used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells which  
CC comprises introducing a gene encoding an accessory molecule ligand (AML)  
CC into the cells so that the AML is expressed on the surface of the cells.  
CC Vectors containing the AML genes can be used in gene therapy for treating  
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can  
CC also be used for vaccination to produce immunity against a virus cell,  
CC bacteria, protein, fungus or neoplasia. (Updated on 17-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 786 BP; 250 A; 166 C; 170 G; 200 T; 0 U; 0 Other;  
  
Query Match 74.4%; Score 642.8; DB 2; Length 786;  
Best Local Similarity 99.7%; Pred. No. 5.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db |||  
QY 138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197  
Db |||  
QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 323  
Db |||  
QY 198 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 257  
Db |||  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db |||  
QY 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 317  
Db |||  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT 443  
Db |||  
QY 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT 377  
Db |||  
QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503  
Db |||



|||||  
Db 378 CATAAGTGAGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437  
QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAAATGGGAAACAGCTGACCGTTAAAAGACA 563  
Db 438 CACCATGAGCAACAACCTTGGTAACCCCTGGAAATGGGAAACAGCTGACCGTTAAAAGACA 497  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623  
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 557  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 683  
Db 558 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 617  
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAACAATCCATTCACTTGGG 743  
Db 618 CAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAACAATCCATTCACTTGGG 677  
QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803  
Db 678 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 737  
QY 804 AGTGAGCCATGGCAGCTGGCTTACGTCCTTTGGCTTACTCAAACTC 849  
Db 738 AGTGAGCCATGGCAGCTGGCTTACGTCCTTTGGCTTACTCAAACTC 783

RESULT 14  
AAV12852

ID AAV12852 standard; cDNA to mRNA; 786 BP.

AC AAV12852;

DT 13-MAY-1998 (first entry)

DE CD40 ligand coding sequence.

XX Leucine zipper; fusion protein production; soluble oligomeric protein;  
KW heterologous mammalian type II transmembrane protein; activated T cell;  
KW heterologous mammalian type I transmembrane protein; antibody production;  
KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 1..786

FT /\*tag= a

PN US5716805-A.

XX 10-FEB-1998.

PF 18-MAY-1995; 95US-00446922.

XX 25-OCT-1991; 91US-00783707.

PR 05-DEC-1991; 91US-00805723.

PR 23-OCT-1992; 92US-00969703.

PR 13-AUG-1993; 93US-00107353.

XX (IMMV ) IMMUNEX CORP.

XX Spriggs MK, Srinivasan S;

XX WPI; 1998-144799/13.

DR P-PSDB; AAW41178.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused to  
PT extracellular region of transmembrane protein.

XX Example 1; Col 19-20; 21pp; English.

XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).

CC The encoded protein can be used in a fusion protein produced using the  
CC method of the invention. The method is for preparing soluble oligomeric  
CC protein by culturing a host cell transfected with a vector for the fusion  
CC protein. The soluble oligomeric proteins comprise a leucine zipper fused  
CC to the N terminus of the extracellular region of a heterologous mammalian  
CC type II transmembrane protein or to the C terminus of the extracellular  
CC region of a heterologous mammalian type I transmembrane protein, where  
CC the leucine zipper is a peptide comprising at least part of AAW41171 or  
CC AAW41172, optionally with conservative amino acid substitutions, provided  
CC that the peptide trimerises in solution. A soluble fusion protein  
CC comprising the leucine zipper of AAW41171 linked to the extracellular  
CC region of CD40-L (a type II transmembrane protein that is found on  
CC activated T cells and acts as a ligand for the B-cell antigen CD40)  
CC stimulates B-cell proliferation and antibody production in a similar  
CC manner to membrane-bound CD40-L. A soluble fusion protein comprising the  
CC leucine zipper of AAW41172 linked to the extracellular region of CD27-L  
CC (a type II transmembrane protein that binds to the lymphocyte antigen  
CC CD27) inhibits binding of CD27c (a fusion protein comprising the  
CC extracellular region of CD27 and a human IgG1 Fc region) to EBV-  
CC transformed B cells expressing CD27-L  
XX  
SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 U; 0 Other;

Query Match 74.4%; Score 642.8; DB 2; Length 786;

Best Local Similarity 99.7%; Pred. No. 5.2e-172;

Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAAGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 263  
Db |||  
Db 138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 197  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 323  
Db |||  
Db 198 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTGAACTGTGAGGA 257  
QY 324 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db |||  
Db 258 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 317  
QY 384 GAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443  
Db |||  
Db 318 GAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 377  
QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db |||  
Db 378 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 437  
QY 504 CACCATGAGCAACAACCTTGGTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAGACA 563  
Db |||  
Db 438 CACCATGAGCAACAACCTTGGTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAGACA 497  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623  
Db |||  
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 557  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 683  
Db |||  
Db 558 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 617  
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAACAATCCATTCACTTGGG 743  
Db |||  
Db 618 CAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAACAATCCATTCACTTGGG 677  
QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803  
Db |||  
Db 678 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 737  
QY 804 AGTGAGCCATGGCAGCTGGCTTACGTCCTTTGGCTTACTCAAACTC 849  
Db |||  
Db 738 AGTGAGCCATGGCAGCTGGCTTACGTCCTTTGGCTTACTCAAACTC 783

RESULT 15

AAQ41506  
ID AAQ41506 standard; DNA; 840 BP.  
XX  
AC AAQ41506;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-AUG-1993 (first entry)  
XX  
DE CD40-L DNA.  
XX  
KW Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;  
KW transmembrane; region; intracellular; soluble; activity; B cell;  
KW proliferation; induction; antibody; secretion; IgE; agonist; antagonist;  
KW binding assay; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 46..831  
FT /\*tag= a  
XX  
PN WO9308207-A1.  
XX  
PD 29-APR-1993.  
XX  
PF 23-OCT-1992; 92WO-US008990.  
XX  
PR 25-OCT-1991; 91US-00783707.  
PR 05-DEC-1991; 91US-00805723.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Armitage RJ, Fanslow WC, Spriggs MK;  
XX  
DR WPI; 1993-152417/18.  
DR P-PSDB; AAR36701.  
XX  
PT New cytokine CD40-L as CD40 agonist and antagonist - is used for treating  
PT allergies, lupus, rheumatoid arthritis, graft-versus-host disease and  
PT insulin-dependent diabetes mellitus.  
XX  
PS Claim 1; Fig 2; 80pp; English.  
XX  
CC This sequence encodes a human CD40-L polypeptide which binds to CD40.  
CC CD40-L is a type II membrane polypeptide which has an extracellular  
CC region at its C-terminus, a transmembrane region and an intracellular  
CC region at its N-terminus. A soluble form of CD40-L lacks the  
CC transmembrane domain. CD40-L activity is mediated by binding with CD40 an  
CC induces B cell proliferation and induction of antibody secretion,  
CC including IgE. Membrane bound CD40-L acts as a CD40 agonist and soluble  
CC CD40-L acts as a CD40 antagonist. CD40-L can be used in a binding assay  
CC to detect cells expressing CD40. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 U; 0 Other;  
  
Query Match 74.4%; Score 642.8; DB 2; Length 840;  
Best Local Similarity 99.7%; Pred. No. 5.3e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
DB || |||||  
183 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242  
  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
DB |||||  
243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
DB |||||  
303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362  
  
QY 384 GAAAGAAAAACAGCTTTTGAATGCAAAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443

Db 363 GAAAGAAAAACAGCTTTTGAATGCAAAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 422  
QY 444 CATAAGTGAGGCCAGCCAGCTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 423 CATAAGTGAGGCCAGCCAGCTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482  
QY 504 CACCATGAGCAACAACCTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563  
Db 483 CACCATGAGCAACAACCTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 542  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602  
QY 624 AGTCCATTATTATAGCCAGCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 683  
Db 603 AGTCCATTATTATAGCCAGCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTACT 662  
QY 684 CAGAGCTGCAAAATACCCAGATTCCGCCAAACCTTTGGGGCAACAATCCATTCACTTTGGG 743  
Db 663 CAGAGCTGCAAAATACCCAGATTCCGCCAAACCTTTGGGGCAACAATCCATTCACTTTGGG 722  
QY 744 AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803  
Db 723 AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 782  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 849  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 828

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	642.8	74.4	786	1 US-08-446-922-3	Sequence 3, Appli
2	642.8	74.4	786	5 PCT-US93-10034-3	Sequence 3, Appli
3	642.8	74.4	840	1 US-07-940-605A-1	Sequence 1, Appli
4	642.8	74.4	840	1 US-08-184-422-7	Sequence 7, Appli
5	642.8	74.4	840	1 US-08-360-923A-1	Sequence 1, Appli
6	642.8	74.4	840	1 US-08-431-055-3	Sequence 3, Appli
7	642.8	74.4	840	2 US-08-690-096-1	Sequence 1, Appli
8	642.8	74.4	840	2 US-08-249-189-11	Sequence 11, Appl
9	642.8	74.4	840	2 US-08-484-624A-11	Sequence 11, Appl
10	642.8	74.4	840	2 US-08-477-733B-11	Sequence 11, Appl
11	642.8	74.4	840	3 US-08-763-995-1	Sequence 1, Appli
12	642.8	74.4	840	3 US-09-088-913A-11	Sequence 11, Appl
13	642.8	74.4	840	3 US-08-589-771B-7	Sequence 7, Appli
14	642.8	74.4	840	3 US-08-769-819-11	Sequence 11, Appl
15	642.8	74.4	840	3 US-08-770-974-11	Sequence 11, Appl
16	642.8	74.4	840	3 US-08-858-197-3	Sequence 3, Appli
17	642.8	74.4	840	3 US-08-770-981-11	Sequence 11, Appl
18	642.8	74.4	840	4 US-09-399-106-11	Sequence 11, Appl
19	642.8	74.4	840	4 US-09-430-448-1	Sequence 1, Appli
20	642.8	74.4	879	4 US-09-645-926A-1	Sequence 1, Appli
21	642.8	74.4	1803	4 US-09-909-595-3	Sequence 3, Appli
22	642.8	74.4	1816	4 US-09-645-926A-5	Sequence 5, Appli
23	636	73.6	929	1 US-08-446-922-10	Sequence 10, Appl
24	636	73.6	929	2 US-08-249-189-20	Sequence 20, Appl
25	636	73.6	929	2 US-08-484-624A-20	Sequence 20, Appl
26	636	73.6	929	2 US-08-477-733B-20	Sequence 20, Appl
27	636	73.6	929	3 US-09-088-913A-20	Sequence 20, Appl

28	636	73.6	929	3 US-08-769-819-20	Sequence 20, Appl
29	636	73.6	929	3 US-08-770-974-20	Sequence 20, Appl
30	636	73.6	929	3 US-08-770-981-20	Sequence 20, Appl
31	636	73.6	929	4 US-09-399-106-20	Sequence 20, Appl
32	635.2	73.5	1425	2 US-08-249-189-15	Sequence 15, Appl
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36	635.2	73.5	1425	3 US-08-769-819-15	Sequence 15, Appl
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38	635.2	73.5	1425	3 US-08-770-981-15	Sequence 15, Appl
39	635.2	73.5	1425	4 US-09-399-106-15	Sequence 15, Appl
40	627.6	72.6	839	4 US-09-023-655-919	Sequence 919, App
41	497.2	57.5	780	4 US-09-322-409-75	Sequence 75, Appl
42	497.2	57.5	780	4 US-09-322-409-76	Sequence 76, Appl
43	497.2	57.5	780	4 US-09-451-527-75	Sequence 76, Appl
44	497.2	57.5	780	4 US-09-451-527-76	Sequence 76, Appl
45	497.2	57.5	885	4 US-09-322-409-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-08-446-922-3  
; Sequence 3, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 786 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; STRAIN: CD40-L  
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..783
US-08-446-922-3

Query Match 74.4%; Score 642.8; DB 1; Length 786;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 197
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTGAGGA 323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
198 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTGAGGA 257
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 317
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 377
QY 444 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
378 CATAAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 437
QY 504 CACCATGAGCAACAACTTGGTAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
438 CACCATGAGCAACAACTTGGTAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 497
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
QY 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGGTAGATTTCGAGAGAAATCTTACT 683
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
558 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGGTAGATTTCGAGAGAAATCTTACT 617
QY 684 CAGAGCTGCAAATACCCACAGTTCGCCAAACCTTGGGGGCAACAATCCATTCACTTGGG 743
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
618 CAGAGCTGCAAATACCCACAGTTCGCCAAACCTTGGGGGCAACAATCCATTCACTTGGG 677
QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
678 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 737
QY 804 AGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 849
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
738 AGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 783
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RESULT 2
PCT-US93-10034-3
; Sequence 3, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
PCT-US93-10034-3

Query Match 74.4%; Score 642.8; DB 5; Length 786;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
138 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 197
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTGAGGA 323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
198 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAAGTGTGAGGA 257
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 317
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 377
QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
378 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 437
QY 504 CACCATGAGCAACAACTTGGTAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
438 CACCATGAGCAACAACTTGGTAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 497
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
QY 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGGTAGATTTCGAGAGAAATCTTACT 683
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
558 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGGTAGATTTCGAGAGAAATCTTACT 617
QY 684 CAGAGCTGCAAATACCCACAGTTCGCCAAACCTTGGGGGCAACAATCCATTCACTTGGG 743
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
618 CAGAGCTGCAAATACCCACAGTTCGCCAAACCTTGGGGGCAACAATCCATTCACTTGGG 677
QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
678 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 737
QY 804 AGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 849
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
738 AGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 783
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QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849  
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Db 738 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 783

RESULT 3

US-07-940-605A-1  
; Sequence 1, Application US/07940605A  
; Patent No. 5540926  
; GENERAL INFORMATION:  
; APPLICANT: ARUFFO, ALEJANDRO  
; APPLICANT: HOLLENBAUGH, DIANE  
; APPLICANT: LEDBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,605A  
; FILING DATE: 04-SEP-1992  
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 22..807  
US-07-940-605A-1

Query Match 74.4%; Score 642.8; DB 1; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGGAAATCTTCATGAAGATTTTGTATTTCAT 263  
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Db 159 TCATAGAAGGTTGGACAAGATAGAAGGAAATCTTCATGAAGATTTTGTATTTCAT 218  
  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
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Db 219 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278  
  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
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Db 279 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 338  
  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443  
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Db 339 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 398  
  
QY 444 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 503  
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Db 399 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 458  
  
QY 504 CACCATGAGCAACAACCTTGGTAAACCTTGGAAAAATGGGAACAGCTGACCGTTAAAGACA 563  
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Db 459 CACCATGAGCAACAACCTTGGTAAACCTTGGAAAAATGGGAACAGCTGACCGTTAAAGACA 518  
  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
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QY 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGTATGAGAGAAATCTTACT 683  
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Db 579 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGTATGAGAGAAATCTTACT 638  
  
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Db 699 AGGAGTATTGAATTGCAACCAGGTGCTTCGGTGTTCCTTTGGCTTACTCAAACTC 758  
  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 849  
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Db 759 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 804

RESULT 4

US-08-184-422-7  
; Sequence 7, Application US/08184422  
; Patent No. 5565321  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY  
; APPLICANT: FANSHAW, WILLIAM  
; APPLICANT: RENSHAW, BLAIR  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: WIDMER, MICHAEL  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
; TITLE OF INVENTION: IN A CD40 LIGAND GENE  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: MS Word for Apple 5.1, Version a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/184,422  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/009,258  
; FILING DATE: 01/22/93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERKINS, PATRICIA ANNE  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2810-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606

; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear



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; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-184-422-7

Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db 363 GAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 683
Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 662

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGGGGCAACAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGGGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTTGAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAAGCCA 782

QY 804 AGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACTC 828
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RESULT 5
US-08-360-923A-1
; Sequence 1, Application US/08360923A
; Patent No. 5674492
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: LONGO, DAN L.
; APPLICANT: MURPHY, WILLIAM
; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
; TITLE OF INVENTION: EXPRESSING CD40
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; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,923A
; FILING DATE: December 21, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/172,664
; FILING DATE: December 23, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2818-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-360-923A-1
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Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db 363 GAAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA 542
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QY	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	623
Db	543	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	602
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	683
Db	603	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	662
QY	684	CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTCGGGGCAACAATCCATTCACTTGGG	743
Db	663	CAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTCGGGGCAACAATCCATTCACTTGGG	722
QY	744	AGGAGTATTTGAATTGCAACCAAGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAGCCA	803
Db	723	AGGAGTATTTGAATTGCAACCAAGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAGCCA	782
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC	849
Db	783	AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC	828

## RESULT 6

US-08-431-055-3  
; Sequence 3, Application US/08431055  
; Patent No. 5817516  
; GENERAL INFORMATION:  
; APPLICANT: KEHRY, MERILYN R  
; APPLICANT: CASTLE, BRIAN E  
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 100 NEW YORK AVE. N.W. SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431.055

Query Match	74.4%	Score 642.8;	DB 1;	Length 840;
Best Local Similarity	99.7%	Pred. NO. 1.2e-172;		
Matches 644; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	204	TCCAAGAAGGTTGGACAAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263
Db	159	TCATAGAAGGTTGGACAAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	218
QY	264	GAAAAACGATACAGAGATGCAACACACAGGAGAAAAGATCCTTATCCTTACTGAACCTGTGAGGA	323
Db	219	GAAAAACGATACAGAGATGCAACACACAGGAGAAAAGATCCTTATCCTTACTGAACCTGTGAGGA	278
QY	324	GATTAATAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	383
Db	279	GATTAATAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	338
QY	384	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443
Db	339	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	398
QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503
Db	399	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	458
QY	504	CACCATGAGCAACAACTTGGTAAACCCCTGGAAAAATGGGAAACACAGCTGACCCGTTAAAAAGACA	563
Db	459	CACCATGAGCAACAACTTGGTAAACCCCTGGAAAAATGGGAAACACAGCTGACCCGTTAAAAAGACA	518
QY	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA	623
Db	519	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA	578
QY	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	683
Db	579	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	638
QY	684	CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAAATCCATTCACTTGGG	743
Db	639	CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAAATCCATTCACTTGGG	698
QY	744	AGGAGTATTTGAAATGCAACCAGGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAAGCCA	803
Db	699	AGGAGTATTTGAAATGCAACCAGGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAAGCCA	758
QY	804	AGTGAGCCATGGCACTGGCTTTCACGTCTCTTTGGCTTACTCAAACTC	849
Db	759	AGTGAGCCATGGCACTGGCTTTCACGTCTCTTTGGCTTACTCAAACTC	804

## RESULT 7

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US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 07/940,605

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; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
US-08-690-096-1
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Query Match 74.4%; Score 642.8; DB 2; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263
Db 159 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 218

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 219 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278

QY 324 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTAAGGATGTAATGTTAAACAAAGAGGAGCGAA 383
Db 279 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTAAGGATGTAATGTTAAACAAAGAGGAGCGAA 338

QY 384 GAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCACATGT 443
Db 339 GAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCACATGT 398

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db 399 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 458

QY 504 CACCATGAGCAACAACTTGGTAAACCTTGGAATAATGGGAACAGCTGACCGTTAAAGACA 563
Db 459 CACCATGAGCAACAACTTGGTAAACCTTGGAATAATGGGAACAGCTGACCGTTAAAGACA 518

QY 564 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTTCAATCGGGAAGCTTCGAGTCA 623
Db 519 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTTCAATCGGGAAGCTTCGAGTCA 578

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 683
Db 579 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 638

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGGCGGCAACATCCATTCTGGG 743
Db 639 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGGCGGCAACATCCATTCTGGG 698

QY 744 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803
Db 699 AGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 758

QY 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 849
Db 759 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 804
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RESULT 8  
US-08-249-189-11  
; Sequence 11, Application US/08249189

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; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-249-189-11
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Query Match 74.4%; Score 642.8; DB 2; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
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QY	324	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383
DB	303	GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	362
QY	384	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443
DB	363	GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	422
QY	444	CATAAGTGAGGCCAGCAGTAAACAAATCTGTGTGTACAGTGGGCTGAAAAGGATACTA	503
DB	423	CATAAGTGAGGCCAGCAGTAAACAAATCTGTGTGTACAGTGGGCTGAAAAGGATACTA	482
QY	504	CACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563
DB	483	CACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	542
QY	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	623
DB	543	AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA	602
QY	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	683
DB	603	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	662
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	743
DB	663	CAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	722
QY	744	AGGAGTATTTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA	803
DB	723	AGGAGTATTTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA	782
QY	804	AGTGAGCCATGGCAGTGGCTTCACTGCTCTTGGCTTACTCAAACCTC	849
DB	783	AGTGAGCCATGGCAGTGGCTTCACTGCTCTTGGCTTACTCAAACCTC	828

## RESULT 9

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US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,624A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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Db 663 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGGGGGCAACAATCCATTCACTTGGG 722  
QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCATGTGACTGATCCAAAGCCA 803  
Db 723 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCATGTGACTGATCCAAAGCCA 782  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 849  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 828

RESULT 10  
US-08-477-733B-11  
; Sequence 11, Application US/08477733B  
; Patent No. 5981724  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,733B  
; FILING DATE: June 07, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,189  
; FILING DATE: May 24, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO

; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
US-08-477-733B-11  
Query Match 74.4%; Score 642.8; DB 2; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGTTGGACAAGATAGAAAGATGAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263  
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGATGAAGGAATCTTTCATGAAGATTTTGTATTTCAT 242  
QY 264 GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323  
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QY 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
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QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAAGGATACTA 503  
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAAGGATACTA 482  
QY 504 CACCATGAGCAACAACTTGGTAAACCTTGGAAATCGGAAACACAGCTGACCCGTTAAAAAGACA 563  
Db 483 CACCATGAGCAACAACTTGGTAAACCTTGGAAATCGGAAACACAGCTGACCCGTTAAAAAGACA 542  
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAAATCGGGAAGCTTCGAGTCA 623  
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAAATCGGGAAGCTTCGAGTCA 602  
QY 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCTTACT 683  
Db 603 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCTTACT 662  
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTTCGGGGCAACAATCCATTCACTTGGG 743  
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTTCGGGGCAACAATCCATTCACTTGGG 722  
QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCGTTCAATGTGACTGATCCAAAGCCA 803  
Db 723 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTCGTTCAATGTGACTGATCCAAAGCCA 782  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 849  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 828

RESULT 11  
US-08-763-995-1  
; Sequence 1, Application US/08763995  
; Patent No. 6017527  
; GENERAL INFORMATION:  
; APPLICANT: MARASKOVSKY, EUGENE  
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA

ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,995  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/677,762  
FILING DATE: 10 JUL 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-763-995-1

Query Match 74.4%; Score 642.8; DB 3; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGATTCAT 263  
|||  
Db 183 TCATAGAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGATTCAT 242  
  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGAGGA 323  
|||  
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGAGGA 302  
  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGTTAAACAAAGAGGACGAA 383  
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Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGTTAAACAAAGAGGACGAA 362  
  
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Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT 422  
  
QY 444 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503  
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Db 423 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 482  
  
QY 504 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563  
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Db 483 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 542  
  
QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
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Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602  
  
QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 683  
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Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 662  
  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTCGGGGCAACAATCCATTCACTTGGG 743  
|||  
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTCGGGGCAACAATCCATTCACTTGGG 722  
|||  
QY 744 AGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCCAAGCCA 803  
|||  
Db 723 AGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCCAAGCCA 782  
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QY 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC 849  
|||  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC 828  
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RESULT 12  
US-09-088-913A-11  
; Sequence 11, Application US/09088913A  
; Patent No. 6087329  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,913A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA



; HYPOTHETICAL: NO									
; ANTI-SENSE: NO									
; ORIGINAL SOURCE:									
; ORGANISM: Homo sapiens									
; IMMEDIATE SOURCE:									
; CLONE: CD40-L									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: 46..831									
US-09-088-913A-11									
Query Match									
Best Local Similarity 74.4%; Score 642.8; DB 3; Length 840;									
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	204	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	263						
Db	183	TCATAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	242						
QY	264	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA	323						
Db	243	GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA	302						
QY	324	GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTATAACAAAGAGGAGACGAA	383						
Db	303	GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTATAACAAAGAGGAGACGAA	362						
QY	384	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT	443						
Db	363	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT	422						
QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503						
Db	423	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482						
QY	504	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGCA	563						
Db	483	CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGCA	542						
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	623						
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	602						
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTTACT	683						
Db	603	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCTTTACT	662						
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTCGGGCAACAATCCATTCACTTGGG	743						
Db	663	CAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTCGGGCAACAATCCATTCACTTGGG	722						
QY	744	AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTCGTTGTCAATGTGACTGATCCAAGCCA	803						
Db	723	AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTCGTTGTCAATGTGACTGATCCAAGCCA	782						
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTTACTCAAACTC	849						
Db	783	AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTTACTCAAACTC	828						



APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,974  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-770-974-11

Query Match 74.4%; Score 642.8; DB 3; Length 840;  
Best Local Similarity 99.7%; Pred. No. 1.2e-172;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGATTCAT 263  
|||  
Db 183 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGATTCAT 242  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323  
|||  
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 383  
|||

Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGAGACGAA 362  
QY 384 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGT 443  
|||  
Db 363 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGT 422  
QY 444 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGTGAAAAAGGATACTA 503  
|||  
Db 423 CATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGTGAAAAAGGATACTA 482  
QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 563  
|||  
Db 483 CACCATGAGCAACAACCTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 542  
QY 564 AGGACTCTATTATATCTATATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
|||  
Db 543 AGGACTCTATTATATCTATATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602  
QY 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 683  
|||  
Db 603 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGGTAGATTTCGAGAGAACTCTTACT 662  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGCGGGCAACAATCCATTCACTTGGG 743  
|||  
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGCGGGCAACAATCCATTCACTTGGG 722  
QY 744 AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803  
|||  
Db 723 AGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 782  
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 849  
|||  
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 828

Search completed: November 12, 2004, 12:57:45  
Job time : 52.6251 secs





Db 806 CTGATCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTAT 865  
QY 260 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTG 319  
Db 866 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTG 925  
QY 320 AGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 379  
Db 926 AGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 985  
QY 380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCAC 439  
Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCAC 1045  
QY 440 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 499  
Db 1046 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 1105  
QY 500 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 559  
Db 1106 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 1165  
QY 560 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 619  
Db 1166 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1225  
QY 620 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 679  
Db 1226 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1285  
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 739  
Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 1345  
QY 740 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 799  
Db 1346 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 1405  
QY 800 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 859  
Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 1465  
QY 860 CTAGA 864  
Db 1466 CTAGA 1470

RESULT 2  
US-10-207-655-149  
; Sequence 149, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 149  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mouse-Human hybrid fusion protein  
US-10-207-655-149  
Query Match 76.8%; Score 663.4; DB 15; Length 1470;  
Best Local Similarity 99.8%; Pred. No. 2e-175;  
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 200 CGGATCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTAT 259

Db 806 CTGATCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTAT 865  
QY 260 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTG 319  
Db 866 TCATGAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTG 925  
QY 320 AGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 379  
Db 926 AGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 985  
QY 380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCAC 439  
Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGGCAC 1045  
QY 440 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 499  
Db 1046 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 1105  
QY 500 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 559  
Db 1106 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 1165  
QY 560 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 619  
Db 1166 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1225  
QY 620 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 679  
Db 1226 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1285  
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 739  
Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 1345  
QY 740 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 799  
Db 1346 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 1405  
QY 800 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 859  
Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 1465  
QY 860 CTAGA 864  
Db 1466 CTAGA 1470

RESULT 3  
US-10-053-530-21  
; Sequence 21, Application US/10053530  
; Publication No. US20030133939A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey  
; APPLICANT: Hayden-Ledbetter, Martha  
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 390069.401  
; CURRENT APPLICATION NUMBER: US/10/053,530  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 09/765,208  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MOUSE-HUMAN HYBRID  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(808)  
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV  
; NAME/KEY: misc\_feature

LOCATION: (814)..(1455)  
OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154  
US-10-053-530-21

Query Match  
Best Local Similarity 76.8%; Score 663.4; DB 15; Length 1470;  
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

200 CGGATCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTGTAT 259  
|||  
806 CTGATCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTGTAT 865  
|||

260 TCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTG 319  
|||  
866 TCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTG 925  
|||

320 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 379  
|||  
926 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 985  
|||

380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 439  
|||  
986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 1045  
|||

440 ATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAGGAT 499  
|||  
1046 ATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAGGAT 1105  
|||

500 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATGGGAAACAGCTGACCGTTAAAA 559  
|||  
1106 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATGGGAAACAGCTGACCGTTAAAA 1165  
|||

560 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 619  
|||  
1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1225  
|||

620 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 679  
|||  
1226 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 1285  
|||

680 TACTCAGAGCTGCAATACCCACAGTTCGCCCAACCTTCGGGGCAACAATCCATTCACT 739  
|||  
1286 TACTCAGAGCTGCAATACCCACAGTTCGCCCAACCTTCGGGGCAACAATCCATTCACT 1345  
|||

740 TGGGAGGAGTATTGAAATGCAACACAGGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 799  
|||  
1346 TGGGAGGAGTATTGAAATGCAACACAGGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 1405  
|||

800 GCCAAGTGAGCCATGGCCTTCACGCTTCCTTTGGCTTACTCAAACTCGAGTGATAAT 859  
|||  
1406 GCCAAGTGAGCCATGGCCTTCACGCTTCCTTTGGCTTACTCAAACTCGAGTGATAAT 1465  
|||

860 CTAGA 864  
||||  
1466 CTAGA 1470  
||||

RESULT 4  
US-09-365-940-11  
Sequence 11, Application US/09365940  
Publication No. US20030091564A1  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,940  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-365-940-11

Query Match 74.4%; Score 642.8; DB 10; Length 840;  
Best Local Similarity 99.7%; Pred. No. 9.2e-170;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTGTATTTCAT 263  
|||  
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTGTATTTCAT 242  
|||

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
|||  
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
|||

QY 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
|||  
Db 303 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362  
|||

QY 384 GAAAAGAAAACAGCTTTTGAATGCAAAAAGGATGATCAGAAATCCTCAAAATTCGGGCACATGT 443  
|||



Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503

Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563

Db 483 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623

Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 683

Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 662

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 743

Db 663 CAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803

Db 723 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 782

QY 804 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAACCTC 849

Db 783 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAACCTC 828

RESULT 5

US-10-294-176-1

; Sequence 1, Application US/10294176

; Publication No. US20030077263A1

; GENERAL INFORMATION:

; APPLICANT: MARASKOVSKY, EUGENE

; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMUNEX CORPORATION

; STREET: 51 UNIVERSITY STREET

; CITY: SEATTLE

; STATE: WASHINGTON

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Power Macintosh 7200/90

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/294,176

; FILING DATE: 14-NO. US20030077263A1-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/430,448

; FILING DATE: 29-Oct-1999

; APPLICATION NUMBER: 08/763,995

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2845-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 840 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: CD40-L

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 46..831

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-294-176-1

Query Match 74.4%; Score 642.8; DB 14; Length 840;

Best Local Similarity 99.7%; Pred. No. 9.2e-170;

Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263

Db 183 TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323

Db 243 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302

QY 324 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383

Db 303 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443

Db 363 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503

Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563

Db 483 CACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623

Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 683

Db 603 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 662

QY 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 743

Db 663 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 803

Db 723 AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA 782

QY 804 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAACCTC 849

Db 783 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAACCTC 828

RESULT 6

US-10-200-242-11

; Sequence 11, Application US/10200242

; Publication No. US2003014182A1

; GENERAL INFORMATION:

; APPLICANT: ARMITAGE, Richard, J.

; APPLICANT: FANSLAW, III, William, C.

; APPLICANT: SPRIGGS, Melanie, K.

; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION

; FILE REFERENCE: 2802-N

; CURRENT APPLICATION NUMBER: US/10/200,242

```
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11

Query Match      74.4%; Score 642.8; DB 15; Length 840;
Best Local Similarity 99.7%; Pred. No. 9.2e-170;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db 363 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACTTGTAAACCTTGAAAAAGTGAACCTGACCTGACCGTTAAAAAGACA 563
Db 483 CACCATGAGCAACAACTTGTAAACCTTGAAAAAGTGAACCTGACCTGACCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCTCTGCTGCTAAAGTCCCGGCAACAATCCATTCACTTGGG 743
Db 603 AGCTCCATTATAGCCAGCTCTGCTGCTAAAGTCCCGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803
Db 723 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 782

QY 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC 828
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RESULT 7

US-10-200-242-11

; Sequence 11, Application US/10200242

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; Publication No. US20040006006A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11
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Query Match 74.4%; Score 642.8; DB 16; Length 840;  
Best Local Similarity 99.7%; Pred. No. 9.2e-170;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 302

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 362

QY 384 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443
Db 363 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422

QY 444 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db 423 CATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 482

QY 504 CACCATGAGCAACAACTTGGTAAACCTTGAAAAATGGGAAAAACAGCTGACCGTTAAAAAGACA 563
Db 483 CACCATGAGCAACAACTTGGTAAACCTTGAAAAATGGGAAAAACAGCTGACCGTTAAAAAGACA 542

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602

QY 624 AGCTCCATTATAGCCAGCTCTGCTGCTAAAGTCCCGGCAACAATCCATTCACTTGGG 743
Db 603 AGCTCCATTATAGCCAGCTCTGCTGCTAAAGTCCCGGCAACAATCCATTCACTTGGG 722

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCAACAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCAACAATCCATTCACTTGGG 722

QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803
Db 723 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 782

QY 744 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803
Db 723 AGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 782
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QY 804 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGCTTACTCAAACCTC 849

Dp 783 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGCTTACTCAAACCTC 828

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RESULT 8
US-10-242-212-1
; Sequence 1, Application US/10242212
; Publication No. US20030099644A1
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEEMA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242,212
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/09/645,926
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-212-1

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		74.4%; Score 642.8; DB 14; Length 879;									
		Best Local Similarity 99.7%; Pred. No. 9.4e-170;									
		Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	204	TCCAAGAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTCATGAAGATTTTGTATTCA	263								
DB	159	TCATAGAAGGTTGGACAAGATAGAAGATGAAAAGGAATCTTCATGAAGATTTTGTATTCA	218								
QY	264	GAACACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACGTGTGAGGA	323								
DB	219	GAACACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACGTGTGAGGA	278								
QY	324	GATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA	383								
DB	279	GATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA	338								
QY	384	GAAGGAAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT	443								
DB	339	GAAGGAAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAACTCTCAAATTCGGGCACATGT	398								
QY	444	CATAAGTGAGGCCAGCATGTAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503								
DB	399	CATAAGTGAGGCCAGCATGTAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	458								
QY	504	CACCATGAGCAACAACCTTGTTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAGACA	563								
DB	459	CACCATGAGCAACAACCTTGTTAAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAAGACA	518								
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA	623								
DB	519	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA	578								
QY	624	AGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	683								
DB	579	AGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	638								
QY	684	CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	743								
DB	639	CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG	698								
QY	744	AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAGCCA	803								
DB	699	AGGAGTATTGTAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAAGCCA	758								
QY	804	AGTGAGCCATGGCACTGGCTTTCACGTCCTTTGGCTTACTCAAACTC	849								

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Db          759 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGCTTACTCAAACTC 804

RESULT 9
US-10-191-997-125
; Sequence 125, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: XM_042961
US-10-191-997-125

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	Query Match Best Local Similarity Matches 644; Conservative	74.4%; 99.7%; 644;	Score 642.8; Pred. No. 1.3e-169; 0;	DB 15; Mismatches 2; Indels 0;	Length 1800; Gaps 0;
QY	204	TCCAAGAAGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTGATTCAT	263		
DB	177	TCATAGAAGTTGGACAAGATAGAAGATGAAAGGAATCTTTCATGAAGATTTTGTGATTCAT	236		
QY	264	GAACACGATACAGAGATGCAACACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA	323		
DB	237	GAACACGATACAGAGATGCAACACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA	296		
QY	324	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAATGTTAAAAACAAAGAGGAGACGAA	383		
DB	297	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAATGTTAAAAACAAAGAGGAGACGAA	356		
QY	384	GAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443		
DB	357	GAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	416		
QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGCTGAAAAAGGATACCTA	503		
DB	417	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGCTGAAAAAGGATACCTA	476		
QY	504	CACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563		
DB	477	CACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	536		
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	623		
DB	537	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	596		
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT	683		
DB	597	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT	656		
QY	684	CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGGGCAACAATCCATTCACTTTGGG	743		
DB	657	CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGGGCAACAATCCATTCACTTTGGG	716		
QY	744	AGGAGTATTTGAATTCGAACCCAGGTGCTTCGGTGTTCATGTGATCTGATCCCAAGCCA	803		
DB	717	AGGAGTATTTGAATTCGAACCCAGGTGCTTCGGTGTTCATGTGATCTGATCCCAAGCCA	776		



QY 804 AGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849  
Db 777 AGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAAACTC 822

RESULT 10  
US-09-909-595-3  
; Sequence 3, Application US/09909595  
; Publication No. US20030083278A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Scott E. Davis  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION  
; FILE REFERENCE: RTS-0223  
; CURRENT APPLICATION NUMBER: US/09/909,595  
; CURRENT FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 3  
; LENGTH: 1803  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (46)...(831)  
US-09-909-595-3

Query Match 74.4%; Score 642.8; DB 10; Length 1803;  
Best Local Similarity 99.7%; Pred. No. 1.3e-169;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 183 TCATAGAAGGTTGGACAAGATAGAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
QY 324 GATTAAAGCCAGTTTGAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db 303 GATTAAAGCCAGTTTGAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443  
Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422  
QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 423 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482  
QY 504 CACCATGAGCAACAACCTTGTTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563  
Db 483 CACCATGAGCAACAACCTTGTTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAGACA 542  
QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 623  
Db 543 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGAGTCA 602  
QY 624 AGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTTTACT 683  
Db 603 AGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAACTTTACT 662  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGCGGGCAACAATCCATTCACTTGGG 743  
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGCGGGCAACAATCCATTCACTTGGG 722  
QY 744 AGGAGTATTGAAATGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCCAAGCCA 803  
Db 723 AGGAGTATTGAAATGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCCAAGCCA 782  
QY 804 AGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849

Db 783 AGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAAACTC 828

RESULT 11  
US-10-272-411-3  
; Sequence 3, Application US/10272411  
; Publication No. US20030100068A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0202  
; CURRENT APPLICATION NUMBER: US/10/272,411  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1803  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATON INFORMATION:  
; DATABASE ACCESSION NUMBER: NCBI/X67878.1  
; DATABASE ENTRY DATE: 1997-06-06  
; RELEVANT RESIDUES: (1)..(1803)  
; PUBLICATON INFORMATION:  
; DATABASE ACCESSION NUMBER: NCBI/X68550.1  
; DATABASE ENTRY DATE: 1993-06-30  
; RELEVANT RESIDUES: (1)..(1803)  
; PUBLICATON INFORMATION:  
; DATABASE ACCESSION NUMBER: NCBI/NM\_000074.1  
; DATABASE ENTRY DATE: 2002-04-10  
; RELEVANT RESIDUES: (1)..(1803)  
; PUBLICATON INFORMATION:  
; DATABASE ACCESSION NUMBER: NCBI/L07414.1  
; DATABASE ENTRY DATE: 1993-04-27  
; RELEVANT RESIDUES: (1)..(1803)  
US-10-272-411-3

Query Match 74.4%; Score 642.8; DB 15; Length 1803;  
Best Local Similarity 99.7%; Pred. No. 1.3e-169;  
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
Db 183 TCATAGAAGGTTGGACAAGATAGAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
Db 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302  
QY 324 GATTAAAGCCAGTTTGAAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
Db 303 GATTAAAGCCAGTTTGAAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 443  
Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCACATGT 422  
QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 503  
Db 423 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA 482  
QY 504 CACCATGAGCAACAACCTTGTTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563  
Db 483 CACCATGAGCAACAACCTTGTTAACCTTGAAAAATGGGAAACAGCTGACCGTTAAAGACA 542  
QY 564 AGGACTCTATTATATCTATGCCCCAAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623

Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	602
QY	624	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT	683
Db	603	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT	662
QY	684	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACCTTGGG	743
Db	663	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACCTTGGG	722
QY	744	AGGAGTATTGAAATTGCAATGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	803
Db	723	AGGAGTATTGAAATTGCAATGCAACCAAGGTGCTTCGGTGTTGTCAATGTGACTGATCCAAAGCCA	782
QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC	849
Db	783	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC	828
RESULT 12			
US-10-218-547-9			
; Sequence 9, Application US/10218547			
; Publication No. US20030100074A1			
; GENERAL INFORMATION:			
; APPLICANT: Human Genome Sciences, Inc.			
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel			
; TITLE OF INVENTION: Human Endokine Alpha			
; FILE REFERENCE: PF561			
; CURRENT APPLICATION NUMBER: US/10/218,547			
; CURRENT FILING DATE: 2002-08-15			
; PRIOR APPLICATION NUMBER: 60/312,542			
; PRIOR FILING DATE: 2001-08-16			
; PRIOR APPLICATION NUMBER: 60/330,761			
; PRIOR FILING DATE: 2001-10-30			
; NUMBER OF SEQ ID NOS: 57			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 9			
; LENGTH: 1803			
; TYPE: DNA			
; ORGANISM: human			
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Query Match 74.4%; Score 642.8; DB 15; Length 1803;			
Best Local Similarity 99.7%; Pred. No. 1.3e-169;			
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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QY	324	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383
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QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503
Db	423	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482
QY	504	CACCATGAGCAACAACCTTGTTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA	563
Db	483	CACCATGAGCAACAACCTTGTTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA	542
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Db	603	AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT	662
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QY	804	AGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC	849
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; Sequence 3, Application US/10272328A			
; Publication No. US20030109444A1			
; GENERAL INFORMATION:			
; APPLICANT: Barnes Jewish Hospital			
; APPLICANT: Lam, Jonathan			
; APPLICANT: Ross, F. Patrick			
; APPLICANT: Teitelbaum, Steven			
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF			
; FILE REFERENCE: 60019620-0206			
; CURRENT APPLICATION NUMBER: US/10/272,328A			
; CURRENT FILING DATE: 2003-01-24			
; PRIOR APPLICATION NUMBER: 60/329,393			
; PRIOR FILING DATE: 2001-10-15			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn version 3.1			
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; TYPE: DNA			
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; PUBLICATION INFORMATION:			
; DATABASE ACCESSION NUMBER: NCBI/X67878.1			
; DATABASE ENTRY DATE: 1997-06-06			
; RELEVANT RESIDUES: (1)..(1803)			
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; PUBLICATION INFORMATION:			
; DATABASE ACCESSION NUMBER: NCBI/L07414.1			
; DATABASE ENTRY DATE: 1993-04-27			
; RELEVANT RESIDUES: (1)..(1803)			
US-10-272-328A-3			
Query Match 74.4%; Score 642.8; DB 15; Length 1803;			
Best Local Similarity 99.7%; Pred. No. 1.3e-169;			
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	204	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263
Db	183	TCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	242
QY	264	GAAAAACGATAACAGAGATGCAACACAGGAGAAAAGATCCTTACTGAACCTGTGAGGA	323
Db	243	GAAAAACGATAACAGAGATGCAACACAGGAGAAAAGATCCTTACTGAACCTGTGAGGA	302
QY	324	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383
Db	303	GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	362
QY	384	GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT	443
Db	363	GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT	422
QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503
Db	423	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482
QY	504	CACCATGAGCAACAACCTTGTTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA	563
Db	483	CACCATGAGCAACAACCTTGTTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAGACA	542
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGAGTCA	623
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGAGTCA	602

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RESULT 14
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; Sequence 15, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: human
US-10-310-793-15
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Query Match 74.4%; Score 642.8; DB 15; Length 1803;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAGGTTGGACACAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263
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Db 183 TCATAGAAGGTTGGACACAGATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 242
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QY 264 GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
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RESULT 15
US-10-202-062-9
; Sequence 9, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 1803
; TYPE: DNA
; ORGANISM: human
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Query Match 74.4%; Score 642.8; DB 16; Length 1803;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db	723	AGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA	782
QY	804	AGTGAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAAACTC	849
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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
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Science 302 (5652), 1960-1963 (2003)  
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering

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1 (bases 1 to 767)



AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCAGGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

FEATURES  
source  
1. .767  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30416146"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCAGGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 66.0%; Score 570; DB 6; Length 767;  
Best Local Similarity 97.8%; Pred. No. 1.6e-148;  
Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
204 TCCAAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 263  
||  
27 TCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 86  
||  
264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323  
||  
87 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 146  
||  
324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383  
||  
147 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 206  
||  
384 GAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAATTCGCGCATGT 443  
||  
207 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAATTCGCGCATGT 266  
||  
444 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503  
||  
267 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 326  
||  
504 CACCATGAGCAACAACTTGGTAAACCCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 563  
||  
327 CACCATGAGCAACAACTTGGTAAACCCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 386  
||  
564 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 623  
||  
387 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTGTTCCAATCGGGAAGCTTCGAGTCA 446  
||

QY 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCTTACT 683  
||  
Db 447 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCTTACT 506  
||  
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGG 743  
||  
Db 507 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGG 566  
||  
QY 744 AGGAGTATTTGAATTGCAACACAGTGCTTCGGTGTGTTGTCATGTGACTGATCCAGCCA 803  
||  
Db 567 AGGAGTATTTGAATTGCAACACAGTGCTTCGGTGTGTTGTC-ATGTGACTGATCCNAGCNA 625  
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RESULT 4  
CD521613 806 bp mRNA linear EST 06-JUN-2003  
LOCUS AGENCOURT 14356206 NIH MGC 191 Homo sapiens cDNA clone  
DEFINITION IMAGE:30413128 5', mRNA sequence.  
ACCESSION CD521613  
VERSION CD521613.1 GI:31453331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 806)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM207 row: j column: 17  
High quality sequence stop: 466.  
Location/Qualifiers  
1. .806  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCAGGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 58.4%; Score 505; DB 6; Length 806;  
Best Local Similarity 96.7%; Pred. No. 2.8e-130;  
Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;  
204 TCCAAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 263  
||  
||

Db 232 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 291

QY 264 GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 323

Db 292 GAAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 351

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383

Db 352 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 411

QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443

Db 412 GAAAGANAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCANATTCGGGCACATGT 471

QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503

Db 472 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 531

QY 504 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 563

Db 532 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 591

QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623

Db 592 AAGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 651

QY 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTTTACT 683

Db 652 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTTTACT 711

QY 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTT-GCGGGCAACAATCCATTCACTTGG 742

Db 712 CAGAGCTGCAAAATACCCCAAGTTCGGCCCAACCTTGGCGGGCAAAACATCCCTTTCCCTTG 771

QY 743 GAG 745

Db 772 GGG 774

RESULT 5  
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LOCUS  
DEFINITION Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY416063  
AY416063.1 GI:397772023  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 783)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 783)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..783  
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gene  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>783  
/gene="TNFSF5"  
/locus\_tag="HCM5765"  
ORIGIN  
Query Match 52.2%; Score 450.8; DB 9; Length 783;  
Best Local Similarity 82.2%; Pred. No. 4.5e-115;  
Matches 531; Conservative 0; Mismatches 112; Indels 3; Gaps 1;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAAGGAATCTTTCATGAAGATTTTGTATTTCAT 263  
Db 138 TCATAGAAGATTGGATAAGGTGGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTTCAT 197  
QY 264 GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323  
Db 198 AAAAAAGCTAAAGAGATGCAACAAAGGAGAGAGGATCTTTATCCTTGTGTAAGTGTGAGGA 257  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 383  
Db 258 GATGAGAAGGCAATTGGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAGA--GAA 314  
QY 384 GAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT 443  
Db 315 AAAAAAAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAAATTGCAGCACACGT 374  
QY 444 CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503  
Db 375 TGTAAGCGAAGCCAAACAGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGGATATTA 434  
QY 504 CACCATGAGCAACAACCTTGGTAAACCCTGGAAAAATGGGAAACAGCTGACCCGTTAAAAAGACA 563  
Db 435 TACCATGAAAAGCAACTTGGTAATGCTTGAAAATGGGAAACAGCTGACCGTTAAAAAGAGA 494  
QY 564 AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
Db 495 AGGACTCTATTATGTCTACACTCAAGTCAACCTTCTGTCTCTAATCGGGAGCCCTTCGAGTCA 554  
QY 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTTTACT 683  
Db 555 ACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCAGCAGTGGATCTGAGAGAACTCTTACT 614  
QY 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGCGGGCAACAATCCATTCACTTGGG 743  
Db 615 CAAGGCGGCAAAATACCCACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGG 674  
QY 744 AGGAGTATTTGAAATGCAACCAGGTGCTTCGGTGTTCGGTGTTCCTCAATGTGACTGATCCAAGCCA 803  
Db 675 CGGAGTGTTTGAAATTACAAGCTGGTGCTTCTGTGTTCCTCAACGCTGACTGAAGCAAGCCA 734  
QY 804 AGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 849  
Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACCTC 780  
RESULT 6  
CD640741  
LOCUS  
DEFINITION CD640741 702 bp mRNA linear EST 17-JUN-2003  
AGENCOURT 14542170 NIH MGC\_191 Homo sapiens cDNA clone  
IMAGE:30414715 5', mRNA sequence.  
CD640741  
CD640741.1 GI:31808911  
EST.  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 702)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDCM211 row: 1 column: 20  
High quality sequence stop: 571.  
Location/Qualifiers

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source  
1. .702  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:30414715"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed  
and directionally cloned. PBMC - Peripheral Blood  
Mononuclear Cells. RNA was pooled from 3/6hour stimulation  
with PMA adn Ionomycin. 5' and 3' adaptors were used in  
cloning as follows: 5' adaptor sequence:  
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.69  
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 46.2%; Score 399.4; DB 6; Length 702;  
Best Local Similarity 95.9%; Pred. No. 1.2e-100;  
Matches 421; Conservative 0; Mismatches 16; Indels 2; Gaps 1;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
|||  
Db 208 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 267  
QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTCTTACTGAACCTGTGAGGA 323  
|||  
Db 268 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTACTCTTACTGAACCTGTGAGGA 327  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTAAACAAAGAGGAGACGAA 383  
|||  
Db 328 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTAAACAAAGAGGAGACGAA 387  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 443  
|||  
Db 388 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 447  
QY 444 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503  
|||  
Db 448 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 507  
QY 504 CACCATGAGCAACAACTTGGTAAACCCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 563  
Db 508 CACCATGAGCAACAACTTGGTAAACCCTGGAAAATGGGAAACAGCTGACCGTTAAAGACA 567  
QY 564 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623  
Db 568 AGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 627  
QY 624 AGCTCCATTTATAGCCAGC 642  
Db 628 --GTCATTATAGCCAGC 644

RESULT 7  
CD642064  
LOCUS  
DEFINITION  
AGENCOURT 14538852 NIH\_MGC\_191 Homo sapiens cDNA clone  
IMAGE:30418744 5', mRNA sequence.  
CD642064  
CD642064.1 GI:31811566  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .690  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30418744"  
/tissue\_type="Pooled"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_191"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed  
and directionally cloned. PBMC - Peripheral Blood  
Mononuclear Cells. RNA was pooled from 3/6hour stimulation  
with PMA adn Ionomycin. 5' and 3' adaptors were used in  
cloning as follows: 5' adaptor sequence:  
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.69  
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 45.7%; Score 395.2; DB 6; Length 690;  
Best Local Similarity 99.0%; Pred. No. 1.7e-99;  
Matches 397; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 204 TCCAAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263  
|||  
Db 213 TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 272  
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA 323  
|||  
Db 273 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA 332  
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTAAACAAAGAGGAGACGAA 383  
|||  
Db 333 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTAAACAAAGAGGAGACGAA 392  
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 443  
|||



Db	393	GAAGAAGAACAGCTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT	452
Qy	444	CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	503
Db	453	CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGANAAGGATACTA	512
Qy	504	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563
Db	513	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	572
Qy	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGCCA	604
Db	573	AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTGCCA	613
RESULT 8			
CD520208			
LOCUS			
DEFINITION	AGENCOURT 14355767 NIH_MGC_191 Homo sapiens cDNA clone	linear	EST 06-JUN-2003
	IMAGE:30412573 5', mRNA sequence.		
ACCESSION	CD520208		
VERSION	CD520208.1	GI:31451926	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 796)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Narayan Bhat cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDCM206 row: c column: 14 High quality sequence stop: 541.		
FEATURES			
source	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:30412573"		
	/tissue_type="Pooled"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/clone_lib="NIH_MGC_191"		
	/note="Vector: pDNR-LIB; site 1: SfiI (ggccattatggcc); site 2: SfiI (ggcgcctcgcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	45.0%;	Score 389;	DB 6; Length 796;
Best Local Similarity	98.3%;	Pred. No. 9.9e-98;	
Matches 403; Conservative	0;	Mismatches 6;	Indels 1; Gaps 1;

Qy	204	TCCAAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263
Db	205	TCATAGAAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	264
Qy	264	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACGTGTGAGGA	323
Db	265	GAAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCCTTACTGAACGTGTGAGGA	324
Qy	324	GATTAAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383
Db	325	GATTAAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	384
Qy	384	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT	443
Db	385	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGT	444
Qy	444	CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA	503
Db	445	CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTNGCTGAAAAAGGATACTA	504
Qy	504	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563
Db	505	CACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA	564
Qy	564	AGGACTCTATTATATCTATGCCCAAGTCA-CCTTCTGTTCCAATCGGGAA	612
Db	565	AGGACTCTATTATATCTATGCCCAAGTCACCCCTTCTGTTCCAATTCGGGA	614
RESULT 9			
CN794193			
LOCUS			
DEFINITION	CN794193 4129335 BARC 8BOV Bos taurus cDNA clone 8BOV_50H03 5', mRNA	571 bp	linear EST 26-MAY-2004
	sequence.		
ACCESSION	CN794193		
VERSION	CN794193.1	GI:47690173	
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 571)		
AUTHORS	Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and Matukumalli,L.K.		
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Richard G. Baumann Bovine Functional Genomics Lab ANRI BLDG 162: BARC-EAST, Beltsville, MD 20705, USA Tel: 3015048604 Fax: 3015048744 Email: <a href="mailto:rbaumann@anri.barc.usda.gov">rbaumann@anri.barc.usda.gov</a> Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt ',' -trim fasta. Vector identified by cross_match using options -minmatch 12 -minscore 18 Plate: 50 row: H column: 03 Seq primer: CCTATTAGGTGACACTATAGAAC High quality sequence stop: 571.		
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	/sex="Female"		
	/tissue_type="Epithelial, Muscle"		
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	/clone_lib="BARC 8BOV"		

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/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
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pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match      33.1%; Score 286.4; DB 7; Length 571;
Best Local Similarity 89.5%; Pred. No. 5.5e-69;
Matches 308; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 506 CCATGACCAACAACCTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACAAG 565
Db 1 CCCTAAGCAACAACCTGGTAACCTCGGAAACGGGAAACAGCTGGCCGTGAAAAGACAAG 60

Qy 566 GACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCAAG 625
Db 61 GATTCTATCACATCTACACCCAAGTCACCTTCTGTTCCAAATCGGGAACCTTTGAGTCAAG 120

Qy 626 CTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACTCA 685
Db 121 CTCCATTTATAGCCAGCCTCTGCCTGAAGTCCCCAAGTGGATCAGAGAGAAATCTTACTGA 180

Qy 686 GAGCTGCAAAATACCCACAGTTCGCCCAACCTTCGCGGCAACAATCCATTCACTTGGGAG 745
Db 181 GAGCTGCAAAACACCCACAGTTCCTCCAAACCATCGCGGCGAGCAATCCATTCACTTAGGAG 240

Qy 746 GAGTATTGAAATTGCAACCAAGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAGCCAAG 805
Db 241 GAGTCTTGAATTGCAATCGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAGTCAAG 300

Qy 806 TGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849
Db 301 TGAGCCACGGGACGGGCTTCACATCATTTGGCTTACTCAAACTC 344

RESULT 10
CK834247      740 bp      mRNA      linear      EST 04-MAR-2004
LOCUS      4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA
DEFINITION      sequence.
ACCESSION      CK834247
VERSION      CK834247.1 GI:45064536
KEYWORDS      EST.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE      1 (bases 1 to 740)
AUTHORS      Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
Matukumalli,L.K.
TITLE      Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim alt -' -trim fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 2 row: M column: 16
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 740.
Location/Qualifiers
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NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match      28.5%; Score 246.4; DB 7; Length 740;
Best Local Similarity 86.9%; Pred. No. 1e-57;
Matches 271; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 204 TCCAAGAAAGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTTGTATTCA 263
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Qy 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACGTGTGAGGA 323
Db 489 GAAAACGATACAGAGATGCAATAAAGGAGAGGGGTCTTATCCTTACTGAACGTGTGAGGA 548

Qy 324 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAATGTTAAACAAAGAGGAGACGAA 383
Db 549 AATTAGAAGCCGTTTGAAGACTTGGTCAAGGATATAATGCAAAACAAAGAGTAAGAA 608

Qy 384 GAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAATTCGCGSCACATGT 443
Db 609 GAAAGAAAACAACTTTGAAATGCACAAAGGTGATCAGGAGCCTCAGATAGCGGCACATGT 668

Qy 444 CATAAGTGAGGCCAGCAGTAAACACATCTGTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db 669 CATCAGTGAGGCCAGTAGTAAACACACCTCTGTCTCCAGTGGGCCCCCAAGGATACTA 728

Qy 504 CACCATGAGCAA 515
Db 729 CACCTTAAGCAA 740

RESULT 11
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LOCUS      263218 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
DEFINITION      BF599437
ACCESSION      BF599437
VERSION      BF599437.1 GI:11695919
KEYWORDS      EST.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE      1 (bases 1 to 492)
AUTHORS      Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
TITLE      Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL      Genome Res. 11 (4), 626-630 (2001)
MEDLINE      21180013
PUBMED      11282978
COMMENT      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
```





REFERENCE	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
AUTHORS					
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.					
1 (bases 1 to 398)					
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	Genome Res. 11 (4), 626-630 (2001)	21180013	11282978	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

ORIGIN	Query Match	19.6%;	Score 169;	DB 2;	Length 398;
	Best Local Similarity	88.0%;	Pred. No. 4.3e-36;		
	Matches 184;	Conservative	0;	Mismatches 25;	Indels 0; Gaps 0;
Qy	204	TCCAAGAAGGTTGGACAAGATAGAAGATGAAAGGAAATCTTTCATGAAGATTTTGTATTTCAT	263		
Db	190	TCACAGAAGATTGGACAAGATAGAAGACGAAGGAAATCTTTCATGAAGATTTTGTGTTCAT	249		
Qy	264	GAACACGATACAGAGATGCAACACAGGAGAAAGATCTCTTATCTTACTGAACCTGTGAGGA	323		
Db	250	GAACACGATACAGAGATGCAATAAAGGAGAGGGGTCTTATCTTACTGAACCTGTGAGGA	309		
Qy	324	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA	383		
Db	310	AATTAGAAGCCGGTTTGAAGACTTGGTCAAGGATATAATGCAAAACAAAGAAGTAAAGAA	369		
Qy	384	GAAGAAAAACAGCTTTGAAATGCAAAAAAG	412		
Db	370	GAAGAAAAAACTTTGAAATGCACAAAG	398		

RESULT 14	CO702364/c	CO702364	636 bp	mRNA	linear	EST 26-JUL-2004
LOCUS		DG32-22804	DG32-liver	Canis familiaris	cdNA 3'	mRNA sequence.
DEFINITION		CO702364				
ACCESSION		CO702364.1	GI:50651032			
VERSION						
KEYWORDS		EST.				
SOURCE		Canis familiaris (dog)				
ORGANISM		Canis familiaris				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
REFERENCE		1 (bases 1 to 636)				

Seq primer: GTAATACGACTCACTATAGGG.  
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Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

ORIGIN

Query Match 12.5%; Score 108.4; DB 7; Length 847;  
Best Local Similarity 91.3%; Pred. NO. 5.5e-19;  
Matches 115; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 724 CAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTC 783  
DB 847 CAGCAATCCATTCACTTAGGAGGAGTCTTTGAATTGCAATCGGGTGCTTCGGTGTTC 788  
QY 784 AATGTGACTGATCCAAAGTCAAGTGAAGTGGCACTGGGCTTCACGTCTTTGGCTTACTC 843  
DB 787 AATGTGACTGATCCAAAGTCAAGTGAAGTGGCACTGGGCTTCACATCATTTGGCTTACTC 728  
QY 844 AAATC 849  
DB 727 AAATC 722

Search completed: November 12, 2004, 12:49:36  
Job time : 1899.8 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 1965.86 Seconds  
(without alignments)  
16453.933 Million cell updates/sec

Title: US-09-687-864A-19  
Perfect score: 684  
Sequence: 1 aagcttgccgccatgtgta.....aactcgagtataatctaga 684

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	68.1	1566	6	AX455878
2	463.6	67.8	786	6	I87864
3	463.6	67.8	786	6	BD064000
4	463.6	67.8	786	6	BD064003
5	463.6	67.8	786	6	BD064005
6	463.6	67.8	786	6	BD064006
7	463.6	67.8	840	6	AR044779
8	463.6	67.8	840	6	AR076926
9	463.6	67.8	840	6	AR078316
10	463.6	67.8	840	6	AR085419
11	463.6	67.8	840	6	AR103375
12	463.6	67.8	840	6	AR106246
13	463.6	67.8	840	6	AR169232
14	463.6	67.8	840	6	AR171647
15	463.6	67.8	840	6	BD190674
16	463.6	67.8	840	6	I23893
17	463.6	67.8	840	6	I27345
18	463.6	67.8	840	6	I67828
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20	463.6	67.8	840	6	AR267621	AR267621 Sequence
21	463.6	67.8	870	9	BC074950	BC074950 Homo sapi
22	463.6	67.8	879	6	AR254616	AR254616 Sequence
23	463.6	67.8	879	6	AX090039	AX090039 Sequence
24	463.6	67.8	879	9	HSGP39MR	Z15017 H.sapiens m
25	463.6	67.8	929	6	AR076932	AR076932 Sequence
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27	463.6	67.8	929	6	AR085425	AR085425 Sequence
28	463.6	67.8	929	6	AR103381	AR103381 Sequence
29	463.6	67.8	929	6	AR169238	AR169238 Sequence
30	463.6	67.8	929	6	I87867	I87867 Sequence 10
31	463.6	67.8	929	6	AR216265	AR216265 Sequence
32	463.6	67.8	1425	6	AR076929	AR076929 Sequence
33	463.6	67.8	1425	6	AR078319	AR078319 Sequence
34	463.6	67.8	1425	6	AR085422	AR085422 Sequence
35	463.6	67.8	1425	6	AR103378	AR103378 Sequence
36	463.6	67.8	1425	6	AR169235	AR169235 Sequence
37	463.6	67.8	1425	6	AR216262	AR216262 Sequence
38	463.6	67.8	1798	6	CQ725625	CQ725625 Sequence
39	463.6	67.8	1803	6	AR350226	AR350226 Sequence
40	463.6	67.8	1803	9	HSCD40	X67878 H.sapiens m
41	463.6	67.8	1816	6	BD187611	BD187611 Screening
42	463.6	67.8	1816	6	BD270930	BD270930 Use of CD
43	463.6	67.8	1816	6	AR254617	AR254617 Sequence
44	463.6	67.8	1816	9	HUMCD40L	L07414 Human CD40-
45	463.6	67.8	1822	9	HSTRAPA	X68550 H.sapiens T

ALIGNMENTS

RESULT 1  
AX455878  
LOCUS AX455878 1566 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 6 from Patent WO0202751.  
ACCESSION AX455878  
VERSION AX455878.1 GI:21714871  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Shirwan,H.  
TITLE Alteration of cell membrane for new functions  
JOURNAL Patent: WO 0202751-A 6 10-JAN-2002;  
UNIVERSITY OF LOUISVILLE RESEARCH FOUNDATION, INC. (US)  
FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match	68.1%;	Score 466;	DB 6;	Length 1566;
Best Local Similarity	98.9%;	Pred. No. 2.4e-116;		
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Qy	200	CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTGCGGCAC	259	
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Qy	260	ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTGAAAAAGGAT	319	
Db	826	ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTGAAAAAGGAT	885	
Qy	320	ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379	
Db	886	ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	945	
Qy	380	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA	439	
Db	946	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA	1005	



QY 440 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499  
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Db 1006 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 1065  
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QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 559  
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Db 1066 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 1125  
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QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619  
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RESULT 2  
187864  
LOCUS 187864 187864 786 bp DNA linear PAT 10-AUG-1998  
DEFINITION Sequence 3 from patent US 5716805.  
ACCESSION 187864  
VERSION 187864.1 GI:3407804  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 786)  
AUTHORS Srinivasan,S. and Spriggs,M.K.  
TITLE Methods of preparing soluble, oligomeric proteins  
JOURNAL Patent: US 5716805-A 3 10-FEB-1998;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 67.8%; Score 463.6; DB 6; Length 786;  
Best Local Similarity 99.1%; Pred. No. 1.1e-115;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGTGAAAAAGGAT 319  
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Db 374 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGTGAAAAAGGAT 433  
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Db 434 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 493  
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QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
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Db 494 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 553  
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QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAAACCTC 669  
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Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAAACCTC 783  
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RESULT 3  
BD064000  
LOCUS BD064000 786 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.  
ACCESSION BD064000  
VERSION BD064000.1 GI:22609603  
KEYWORDS JP 2001505782-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 786)  
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.  
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease  
JOURNAL Patent: JP 2001505782-A 1 08-MAY-2001;  
UNIVERSITY OF CALIFORNIA  
COMMENT PD 08-MAY-2001  
PF 08-DEC-1997 JP 1998526956  
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL  
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/705, C12N15/86,  
PC A61K48/00,A61K38/17,A61K35/12  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
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ORIGIN

Query Match 67.8%; Score 463.6; DB 6; Length 786;  
Best Local Similarity 99.1%; Pred. No. 1.1e-115;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAAACCTC 669  
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Db 734 GCCAAGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAAC TC 783

RESULT 4  
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LOCUS  
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.  
BD064003  
ACCESSION  
VERSION BD064003.1 GI:22609606  
KEYWORDS JP 2001505782-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 786)  
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.  
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease  
JOURNAL Patent: JP 2001505782-A 4 08-MAY-2001;  
COMMENT UNIVERSITY OF CALIFORNIA  
PN JP 2001505782-A/4  
PD 08-MAY-2001  
PF 08-DEC-1997 JP 1998526956  
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI  
THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL  
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/525,C07K14/705,  
PC C12N15/86,  
PC A61K48/00,A61K38/17,A61K35/12  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

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ORIGIN

Query Match 67.8%; Score 463.6; DB 6; Length 786;  
Best Local Similarity 99.1%; Pred. No. 1.1e-115;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259  
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QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 499  
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QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA 619  
Db 674 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAAC TC 669

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RESULT 5  
BD064005  
LOCUS  
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.  
BD064005  
ACCESSION  
VERSION BD064005.1 GI:22609608  
KEYWORDS JP 2001505782-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 786)  
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.  
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease  
JOURNAL Patent: JP 2001505782-A 6 08-MAY-2001;  
COMMENT UNIVERSITY OF CALIFORNIA  
PN JP 2001505782-A/6  
PD 08-MAY-2001  
PF 08-DEC-1997 JP 1998526956  
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI  
THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL  
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/525,C07K14/705,  
PC C12N15/86,  
PC A61K48/00,A61K38/17,A61K35/12  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

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ORIGIN

Query Match 67.8%; Score 463.6; DB 6; Length 786;  
Best Local Similarity 99.1%; Pred. No. 1.1e-115;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259  
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QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGTGAAAAAGGAT 319  
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QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db 434 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 493

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
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Db 614 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACT 673

QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA 619  
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RESULT 6	
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LOCUS	BD064006 786 bp DNA linear PAT 27-AUG-2002
DEFINITION	Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.
ACCESSION	BD064006
VERSION	BD064006.1 GI:22609609
KEYWORDS	JP 2001505782-A/7.
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.

Kipps, T.J., Sharma, S. and Cantwell, M.  
 Novel expression vectors containing accessory molecule ligand genes  
 and their use for immuno-modulation and treatment of malignancies  
 and autoimmune disease  
 Patent: JP 2001505782-A 7 08-MAY-2001;  
 UNIVERSITY OF CALIFORNIA  
 PN JP 2001505782-A/7  
 PD 08-MAY-2001  
 PF 08-DEC-1997 JP 1998526956  
 PR 09-DEC-1996 US 60/032145, 01-DEC-1997 US 08/982272 PI  
 THOMAS J KIPPS, SANJAI SHARMA, MARK CANTWELL  
 PC C12N15/12, C12N15/62, C07K14/48, C07K14/52, C07K14/525, C07K14/705,  
 PC C12N15/86,  
 PC A61K48/00, A61K38/17, A61K35/12  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.  
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 source  
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Qy	620	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAAAC TC	669
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RESULT 7

AR044779

LOCUS

DEFINITION

SEQUENCE 3 from patent US 5817516.

AR044779

ACCESSION

AR044779.1

GI:5966244

KEYWORDS

UNKNOWN.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

AR044779

Sequence 3 from patent US 5817516.

AR044779

AR044779.1

GI:5966244

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Unknown.

Unknown.

Unclassified.

1 (bases 1 to 840)

Kehry,M. and Castle,B.

Methods for proliferating and differentiating B cells with high density membrane CD40 ligand

Patent: US 5817516-A 3 06-OCT-1998;

Location/Qualifiers

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	Best Local Similarity	99.1%;	Pred. No. 1.1e-115;		
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QY	200	CGGATCCAGAAAA	CAGCTTTGAAAATGCAAAAAGGTGATCAGAAATCCTCAAATTTGCGGCAC	259	
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QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
Db	395	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	454		
QY	320	ACTACACCATGAGCAACAACTTTGGTAAACCTTGGAAAAATGGAAACAGCTGACCGTTAAAA	379		
Db	455	ACTACACCATGAGCAACAACTTTGGTAAACCTTGGAAAAATGGAAACAGCTGACCGTTAAAA	514		
QY	380	GACAAGGACTCTATTATATCTATATGCCCAAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439		
Db	515	GACAAGGACTCTATTATATCTATATGCCCAAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	574		
QY	440	GTCGAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCT	499		
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QY	500	TACTCAGAGCTGCAAAATACCAAGTTCCGCCAAACCTTGGCGGGCAACAATCCATTCACT	559		
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DEFINITION	Sequence 11 from patent US 5961974.				
ACCESSION	AR076926				
VERSION	AR076926.1	GI:10003672			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				



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Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS  Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE     Monoclonal antibodies to CD40 ligand, pharmaceutical composition
          comprising the same and hybridomas producing the same
JOURNAL   Patent: US 5961974-A 11 05-OCT-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
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QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAATAATGGGAAACAGCTGACCCGTTAAAA 379
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RESULT 9
AR078316 LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 11 from patent US 5962406.
ACCESSION AR078316
VERSION AR078316.1 GI:10005062
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
        Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE     Recombinant soluble CD40 ligand polypeptide and pharmaceutical
          composition containing the same
JOURNAL   Patent: US 5962406-A 11 05-OCT-1999;
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Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
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QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAATAATGGGAAACAGCTGACCCGTTAAAA 379
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Db 719 TGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTTCCTCAATGTGATCCAA 778
QY 620 GCCAAGTGAGCCATGGCAGTGGCTTACAGTCCCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTGAGCCATGGCAGTGGCTTACAGTCCCTTTGGCTTACTCAAACTC 828

RESULT 9
AR078316 LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 11 from patent US 5962406.
ACCESSION AR078316
VERSION AR078316.1 GI:10005062
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
        Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE     Recombinant soluble CD40 ligand polypeptide and pharmaceutical
          composition containing the same
JOURNAL   Patent: US 5962406-A 11 05-OCT-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
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Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 560 TGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTTCCTCAATGTGATCCAA 619
Db 719 TGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTTCCTCAATGTGATCCAA 778
QY 620 GCCAAGTGAGCCATGGCAGTGGCTTACAGTCCCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTGAGCCATGGCAGTGGCTTACAGTCCCTTTGGCTTACTCAAACTC 828

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DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
        Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE     DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL   Patent: US 5981724-A 11 09-NOV-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
Db 359 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 418
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QY      620  GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 669
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RESULT 11
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DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES
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    Best Local Similarity 99.1%; Pred. No. 1.le-115;
    Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      200  CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259
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QY      260  ATGTCATAAGTGAGGCCAGCAAGTAAACAACATCTGTGTTACAGTGGGTGAAAAAGGAT 319
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QY      320  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA 379
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QY      440  GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
Db      599  GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 658
QY      500  TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db      659  TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 718
QY      560  TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
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RESULT 13
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DEFINITION Sequence 11 from patent US 6290972.
ACCESSION AR169232
VERSION AR169232.1 GI:17907047
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
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Db      779  GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 828

RESULT 12
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DEFINITION Sequence 7 from patent US 6106832.
ACCESSION AR106246
VERSION AR106246.1 GI:12820776
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.
TITLE Treatment of individuals exhibiting defective CD40L
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;
FEATURES
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ORIGIN

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    Best Local Similarity 99.1%; Pred. No. 1.le-115;
    Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      200  CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259
Db      359  CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 418
QY      260  ATGTCATAAGTGAGGCCAGCCAGTAAACAACATCTGTGTTACAGTGGGTGAAAAAGGAT 319
Db      419  ATGTCATAAGTGAGGCCAGCCAGTAAACAACATCTGTGTTACAGTGGGTGAAAAAGGAT 478
QY      320  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA 379
Db      479  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA 538
QY      380  GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db      539  GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
QY      440  GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
Db      599  GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 658
QY      500  TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db      659  TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 718
QY      560  TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db      719  TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778
QY      620  GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 669
Db      779  GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 828

RESULT 13
AR169232 LOCUS AR169232 840 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6290972.
ACCESSION AR169232
VERSION AR169232.1 GI:17907047
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
```





QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	478
QY	320	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379
Db	479	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	538
QY	380	GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAGCTTCGA	439
Db	539	GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAGCTTCGA	598
QY	440	GTCAAGCTCCATTTTATAGCCAGCCTCTGCGCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT	499
Db	599	GTCAAGCTCCATTTTATAGCCAGCCTCTGCGCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT	658
QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGCGGGGCAACAATCCATTCACT	559
Db	659	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGCGGGGCAACAATCCATTCACT	718
QY	560	TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	619
Db	719	TGGGAGGAGTATTGAAATTGCAACCAAGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	778
QY	620	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC	669
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Job time : 1966.86 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 15:28:44 ; Search time 224.368 Seconds  
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Scoring table: IDENTITY\_NUC  
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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	684	100.0	684	4	AAF82935	Aaf82935 HIV-1 gp1
2	630.4	92.2	726	4	AAF82934	Aaf82934 HIV-1 gp1
3	496.2	72.5	2028	4	AAF82931	Aaf82931 HIV-1 gp1
4	494	72.2	865	4	AAF82933	Aaf82933 HIV-1 gp1
5	485	70.9	2070	4	AAF82930	Aaf82930 HIV-1 gp1
6	483.4	70.7	1290	6	ABK89858	Abk89858 Synthetic
7	483.4	70.7	1290	10	ADD25461	Add25461 Binding d
8	483.4	70.7	1290	10	ADD25590	Add25590 Binding d
9	483.4	70.7	1290	11	ADM42736	Adm42736 2H7scFv-C
10	478.6	70.0	906	4	AAF82932	Aaf82932 HIV-1 gp1
11	478.6	70.0	1470	6	ABK89857	Abk89857 Synthetic
12	478.6	70.0	1470	10	ADD25460	Add25460 Binding d
13	478.6	70.0	1470	10	ADD25588	Add25588 Binding d
14	478.6	70.0	1470	11	ADM42735	Adm42735 2H7-CD154
15	478.6	70.0	2209	4	AAF82929	Aaf82929 HIV-1 gp1
16	478.6	70.0	2252	4	AAF82928	Aaf82928 HIV-1 gp1
17	466	68.1	1566	6	ABK12874	Abk12874 Chimeric
18	463.6	67.8	786	2	AAQ63959	Aaq63959 Human CD4
19	463.6	67.8	786	2	AAV39002	Aav39002 Exemplary
20	463.6	67.8	786	2	AAV39000	Aav39000 Exemplary
21	463.6	67.8	786	2	AAV38997	Aav38997 CD40 liga

22	463.6	67.8	786	2	AAV39003	Aav39003 Exemplary
23	463.6	67.8	786	2	AAV12852	Aav12852 CD40 liga
24	463.6	67.8	840	2	AAQ41506	Aaq41506 CD40-L DN
25	463.6	67.8	840	2	AAQ67123	Aaq67123 CD40 liga
26	463.6	67.8	840	2	AAT05763	Aat05763 Human CD4
27	463.6	67.8	840	2	AAT93782	Aat93782 cDNA of C
28	463.6	67.8	840	2	AAV61063	Aav61063 Human CD4
29	463.6	67.8	840	2	AAZ27525	Aaz27525 Human CD4
30	463.6	67.8	840	10	ADH50747	Adh50747 Human CD4
31	463.6	67.8	879	4	AAF55539	Aaf55539 Nucleotid
32	463.6	67.8	929	2	AAT58123	Aat58123 cDNA enco
33	463.6	67.8	929	2	AAZ27537	Aaz27537 Human tri
34	463.6	67.8	929	10	ADH50756	Adh50756 Human tri
35	463.6	67.8	961	10	ADH50763	Adh50763 Human CD4
36	463.6	67.8	1425	2	AAQ41516	Aaq41516 Human CD4
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42	463.6	67.8	1803	8	ACC57894	Acc57894 Human CD4
43	463.6	67.8	1803	10	ADC35191	Adc35191 Human CDN
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ALIGNMENTS

RESULT 1  
AAF82935  
ID AAF82935 standard; cDNA; 684 BP.  
XX  
AC AAF82935;

XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX

DE HIV-1 gp120 V3 loop-CD154 short form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Homo sapiens.

Key	Location/Qualifiers
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WO200126608-A2.

19-APR-2001.

13-OCT-2000; 2000WO-US028414.

14-OCT-1999; 99US-0159690P.

(LEDB/) LEDBETTER J A.

PA	(HAYD/) HAYDEN-LEDBETTER M S.	
XX	Ledbetter JA, Hayden-Ledbetter MS;	
PI		
XX		
DR	WPI; 2001-281790/29.	
DR	P-PSDB; AAB62340.	
XX		
PT	DNA vaccine for improving antigen-specific humoral and cellular immune	
PT	responses, comprising one or more antigens linked to a domain that binds	
PT	at least one receptor.	
XX		
PS	Example 1; Fig 2B; 55pp; English.	
XX		
CC	The invention provides a vaccine comprising one or more antigens linked	
CC	to a domain that binds at least one receptor to improve the antigen-	
CC	specific humoral and cellular immune response. The DNA vaccines induce	
CC	strong antigen-specific humoral and cellular immune responses. The	
CC	vaccine can be use against acquired immunodeficiency syndrome (AIDS). The	
CC	present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human	
CC	CD154 short form extracellular domain fusion protein linked by ProAspPro	
CC	linker. (Updated on 11-SEP-2003 to standardise OS field)	
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SQ	Sequence 684 BP; 216 A; 154 C; 147 G; 167 T; 0 U; 0 Other;	
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Best Local Similarity 100.0%; Pred. No. 1.4e-193;		
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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QY	121 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA	180
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QY	181 GCACATTGTAACATTAGTCCGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAG	240
Db		
QY	241 AATCCTCAAATTGCGGCACATGTCAATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTA	300
Db		
QY	301 CAGTGGGCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGG	360
Db		
QY	361 AAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGT	420
Db		
QY	421 TCCAATCGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCCTCTGCCTAAAGTCCCCC	480
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QY	481 GGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACCTTGC	540
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AC	AAF82934;	
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DT	11-SEP-2003 (revised)	
DT	29-JUN-2001 (first entry)	
XX		
DE	HIV-1 gp120 V3 loop-CD154 short form extracellular domain fusion cDNA.	
XX		
KW	Antigen; receptor; humoral; cellular; immune response; DNA vaccine;	
KW	acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;	
KW	HIV-1; gp120; human; CD154; fusion protein; ss.	
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OS	Human immunodeficiency virus 1.	
OS	Homo sapiens.	
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FT		/*tag= d
FT		/note= "[Gly4Ser]3 linker coding sequence"
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FT		/*tag= e
FT		/note= "human CD154 short form extracellular domain coding sequence"
XX		
PN	WO200126608-A2.	
XX		
PD	19-APR-2001.	
XX		
PF	13-OCT-2000; 2000WO-US028414.	
XX		
PR	14-OCT-1999; 99US-0159690P.	
XX		
PA	(LEDB/) LEDBETTER J A.	
PA	(HAYD/) HAYDEN-LEDBETTER M S.	
PI	Ledbetter JA, Hayden-Ledbetter MS;	
XX		
DR	WPI; 2001-281790/29.	
DR	P-PSDB; AAB62339.	
XX		
PT	DNA vaccine for improving antigen-specific humoral and cellular immune	
PT	responses, comprising one or more antigens linked to a domain that binds	
PT	at least one receptor.	
XX		
PS	Example 1; Fig 2B; 55pp; English.	
XX		
CC	The invention provides a vaccine comprising one or more antigens linked	
CC	to a domain that binds at least one receptor to improve the antigen-	
CC	specific humoral and cellular immune response. The DNA vaccines induce	
CC	strong antigen-specific humoral and cellular immune responses. The	
CC	vaccine can be use against acquired immunodeficiency syndrome (AIDS). The	
CC	present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human	
CC	CD154 short form extracellular domain fusion protein linked by (Gly4Ser)3	
CC	linker. (Updated on 11-SEP-2003 to standardise OS field)	
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SQ	Sequence 726 BP; 220 A; 159 C; 171 G; 176 T; 0 U; 0 Other;	
Query Match 92.2%; Score 630.4; DB 4; Length 726;		



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Best Local Similarity 94.1%; Pred. No. 1.4e-177;
Matches 683; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

Qy 1 AAGCTTGGCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60
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Db 1 AAGCTTGGCGCCATGCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60

Qy 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCCCAACAATACAAGAAGAGTTA 120
   |||||
Db 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCCCAACAATACAAGAAGAGTTA 120

Qy 121 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 180
   |||||
Db 121 TCTATAGGACCGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 180

Qy 181 GCACATTGTAAACATTA-----GT 198
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Db 481 AGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCCGGTAGATTTCGAGAGAATC 540

Qy 499 TTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTTGCGGGCAACAATCCATTCCAC 558
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Db 541 TTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTTGCGGGCAACAATCCATTCCAC 600

Qy 559 TTGGGAGGAGTATTGGAATTGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCA 618
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Qy 619 AGCCAACTGAGCCATGGCAGCTGGCTTCAGTCCTTTGGCTTACTCAAACCTCGAGTGATAA 678
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Qy 679 TCTAGA 684
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Db 721 TCTAGA 726
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RESULT 3
AAF82931
ID AAF82931 standard; cDNA; 2028 BP.
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AC AAF82931;
XX
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX
DE HIV-1 gp120-human CD154 'short form extracellular domain fusion cDNA.
XX
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX
OS Human immunodeficiency virus 1.
OS Homo sapiens.
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XX Key Location/Qualifiers
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FT /*note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /*tag= c
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FT misc_feature 1543..1551
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FT /*note= "ProAspPro linker coding sequence"
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FT /*note= "human CD154 short form extracellular domain coding sequence"
FT
XX WO200126608-A2.
XX 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028414.
XX
PR 14-OCT-1999; 99US-0159690P.
XX
PA (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
XX
PI Ledbetter JA, Hayden-Ledbetter MS;
XX
DR WPI; 2001-281790/29.
DR P-PSDB; AAB62336.
XX
PT DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
PS Example 1; Fig 3B; 55pp; English.
XX
CC The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC short form extracellular domain fusion protein linked by a ProAspPro
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
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SQ Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;

Query Match 72.5%; Score 496.2; DB 4; Length 2028;
Best Local Similarity 92.4%; Pred. No. 2.5e-137;
Matches 522; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Db 1464 ATATAAAGTAGTAAGAATTGAACCAATAGGAGTAGCACCCAGGCAAGAGAAGAAC 1523

Qy 180 AGCACATTGTAACATTAGTCCGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCA 239
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Db 1524 AGTGCAAGAGAAAAAGACCGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCA 1583

Qy 240 GAATCCTCAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTT 299
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Db 1584 GAATCCTCAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTT 1643

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   |||||
Db 1644 ACAGTGGGCTGAAAAAGGATACTACCATGAGCAACAACCTTGGTAACCCCTGGAATGG 1703

Qy 360 GAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTG 419
   |||||
```

Db 1704 GAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTG 1763

QY 420 TTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATPAGCCAGCCTCTGCCTAAAGTCCCC 479

Db 1764 TTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATPAGCCAGCCTCTGCCTAAAGTCCCC 1823

QY 480 CGGTAGATTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCGCCAAACCTTG 539

Db 1824 CGGTAGATTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCGCCAAACCTTG 1883

QY 540 CGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGT 599

Db 1884 CGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGT 1943

QY 600 TGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTT 659

Db 1944 TGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTT 2003

QY 660 ACTCAAACTCGAGTGATAATCTAGA 684

Db 2004 ACTCAAACTCGAGTGATAATCTAGA 2028

RESULT 4

AAF82933 ID AAF82933 standard; cDNA; 865 BP.

XX AC AAF82933;

XX DT 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX DE HIV-1 gp120 V3 loop-CD154 long form extracellular domain fusion cDNA.

XX KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

KW HIV-1; gp120; human; CD154; fusion protein; ss.

XX OS Human immunodeficiency virus 1.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 13..865

FT sig\_peptide /\*tag= a

FT /\*tag= b

FT /\*tag= c

FT /\*tag= d

FT /\*tag= e

FT /\*tag= f

FT /\*tag= g

FT /\*tag= h

FT /\*tag= i

FT /\*tag= j

FT /\*tag= k

FT /\*tag= l

FT /\*tag= m

FT /\*tag= n

FT /\*tag= o

FT /\*tag= p

FT /\*tag= q

FT /\*tag= r

FT /\*tag= s

FT /\*tag= t

FT /\*tag= u

FT /\*tag= v

FT /\*tag= w

FT /\*tag= x

FT /\*tag= y

FT /\*tag= z

FT /\*tag= AA

FT /\*tag= AB

FT /\*tag= AC

FT /\*tag= AD

FT /\*tag= AE

FT /\*tag= AF

FT /\*tag= AG

FT /\*tag= AH

FT /\*tag= AI

XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.

PS Example 1; Fig 2A; 55pp; English.

XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human CD154 long form extracellular domain fusion protein linked by ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 865 BP; 290 A; 174 C; 192 G; 209 T; 0 U; 0 Other;

SQ

Query Match 72.2%; Score 494; DB 4; Length 865;  
Best Local Similarity 79.2%; Pred. No. 8e-137;  
Matches 684; Conservative 0; Mismatches 0; Indels 180; Gaps 1;

QY 1 AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60

Db 1 AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60

QY 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCACCAACAATAACAAGAAAGTTA 120

Db 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCACCAACAATAACAAGAAAGTTA 120

QY 121 TCTATAGGACCAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 180

Db 121 TCTATAGGACCAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 180

QY 181 GCACATTGTAACATTAGTCCGGATCC----- 206

Db 181 GCACATTGTAACATTAGTCCGGATCCAAAGAGTTGGACAAGATAGAAGATGAAGGAAT 240

QY 207 ----- 206

Db 241 CTTTCATGAAGATTTTGTATTTCATGAAAACGATACAGATGCAACACAGGAGAAAGATCC 300

QY 207 ----- 206

Db 301 TTATCCTTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATA 360

QY 207 -----AGAAAACAGCTTTGAAATGCAAAAAGGTGATCAG 240

Db 361 ATGTTAAACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAG 420

QY 241 AATCCTCAAATTTGCGGCACATGTATAGTGAGGCCAGCAGTAAACACATCTGTGTTA 300

Db 421 AATCCTCAAATTTGCGGCACATGTATAGTGAGGCCAGCAGTAAACACATCTGTGTTA 480

QY 301 CAGTGGGCTGAAAAGGATACACTACACCATGAGCAACAACCTGGTAAACCTGGAAAATGGG 360

Db 481 CAGTGGGCTGAAAAGGATACACTACACCATGAGCAACAACCTGGTAAACCTGGAAAATGGG 540

QY 361 AAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGT 420

Db 541 AAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGT 600

QY 421 TCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCC 480

Db 601 TCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCC 660

QY 481 GGTAGATTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGC 540

Db 661 GGTAGATTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGC 720

QY 541 GGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGT 600

Db 721 GGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGT 780

Qy 601 GTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTA 660  
|||||  
Db 781 GTCAATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTA 840  
661 CTCAAACTCGAGTGATAATCTAGA 684  
841 CTCAAACTCGAGTGATAATCTAGA 864

RESULT 5  
AAF82930  
ID AAF82930 standard; cDNA; 2070 BP.  
XX  
AC AAF82930;  
XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX  
DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.  
XX  
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..2070  
FT /\*tag= a  
FT sig\_peptide 13..72  
FT /\*tag= b  
FT /note= "synthetic secretory signal peptide"  
FT misc\_feature 73..1542  
FT /\*tag= c  
FT /note= "HIV-1 gp120 domain coding sequence"  
FT misc\_feature 1543..1593  
FT /\*tag= d  
FT /note= "[Gly4Ser]3 linker coding sequence"  
FT misc\_feature 1594..2070  
FT /\*tag= e  
FT /note= "human CD154 short form extracellular domain coding sequence"

WO200126608-A2.  
19-APR-2001.  
13-OCT-2000; 2000WO-US028414.  
14-OCT-1999; 99US-0159690P.  
(LEDB/) LEDBETTER J A.  
(HAYD/) HAYDEN-LEDBETTER M S.  
PI Ledbetter JA, Hayden-Ledbetter MS;  
XX WPI; 2001-281790/29.  
DR P-PSDB; AAB62335.  
XX  
PT DNA vaccine for improving antigen-specific humoral and cellular immune  
PT responses, comprising one or more antigens linked to a domain that binds  
PT at least one receptor.  
XX  
PS Example 1; Fig 3B; 55pp; English.  
XX  
CC The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154

CC short form extracellular domain fusion protein linked by (Gly4Ser)3  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;  
Query Match 70.9%; Score 485; DB 4; Length 2070;  
Best Local Similarity 100.0%; Pred. No. 5.5e-134;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259  
|||||  
Db 1586 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 1645  
Qy 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 319  
|||||  
Db 1646 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 1705  
Qy 320 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA 379  
|||||  
Db 1706 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA 1765  
Qy 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
|||||  
Db 1766 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1825  
Qy 440 GTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499  
|||||  
Db 1826 GTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1885  
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559  
|||||  
Db 1886 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 1945  
Qy 560 TGGGAGGAGTATTTGAAATGCAACCAGGTGCTTCGGTGTGTCAATGTGACTGATCCAA 619  
|||||  
Db 1946 TGGGAGGAGTATTTGAAATGCAACCAGGTGCTTCGGTGTGTCAATGTGACTGATCCAA 2005  
Qy 620 GCCAAGTGAGCCCATGGCACTGGCTTCAACGCTCTTTGGCTTACTCAAACCTCGAGTGATAAT 679  
|||||  
Db 2006 GCCAAGTGAGCCCATGGCACTGGCTTCAACGCTCTTTGGCTTACTCAAACCTCGAGTGATAAT 2065  
Qy 680 CTAGA 684  
Db 2066 CTAGA 2070

RESULT 6  
ABK89858  
ID ABK89858 standard; DNA; 1290 BP.  
XX  
AC ABK89858;  
XX  
DT 05-NOV-2002 (first entry)  
DE Synthetic mouse/human chimeric fusion gene #6.  
XX  
KW Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;  
KW neuroprotective; gene therapy; single chain antibody; variable fragment;  
KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;  
KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;  
KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;  
KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;  
KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;  
KW ulcerative colitis; inflammatory bowel disease; immunological effector;  
KW cell mediated cytotoxicity; complement dependent cytotoxicity;  
KW complement fixation; gene; ds; mouse; human.  
XX  
OS Mus musculus.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers



FT	misc_feature	1..808	
FT	/*tag= b		
FT	/note= "Murine anti-human CD20 single chain antibody		
FT	variable fragment (scFv)"		
FT	CDS	13..1281	
FT	/*tag= a		
FT	/product= "Mouse/human chimeric fusion protein"		
FT	misc_feature	814..1275	
FT	/*tag= c		
FT	/note= "Human extracellular domain short form CD154"		
XX			
PN	WO200256910-A1.		
XX			
PD	25-JUL-2002.		
XX			
PF	17-JAN-2002; 2002WO-US001487.		
XX			
PR	17-JAN-2001; 2001US-00765208.		
XX			
PA	(GENE-) GENE-CRAFT INC.		
XX			
PI	Ledbetter JA, Hayden-Ledbetter M;		
XX			
DR	WPI; 2002-599691/64.		
DR	P-PSDB; ABG31032.		
XX			
PT	New human binding domain-immunoglobulin fusion protein useful for		
PT	treating a subject having or suspected of having a B-cell disorder or		
PT	malignant condition e.g. rheumatoid arthritis.		
XX			
PS	Disclosure; Fig 7C-D; 136pp; English.		
XX			
CC	The invention describes a binding domain-immunoglobulin fusion protein		
CC	that is capable of at least one immunological activity, comprising a		
CC	binding domain polypeptide fused to an immunoglobulin hinge region		
CC	polypeptide capable of specifically binding to an antigen, or an		
CC	immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused		
CC	to the hinge region polypeptide or to the CH2 constant region		
CC	polypeptide. The fusion protein is useful for treating a subject having		
CC	or suspected of having a B-cell disorder or malignant condition e.g.		
CC	rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's		
CC	thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus		
CC	erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,		
CC	psoriasis, scleroderma, cancer and inflammatory bowel disease such as		
CC	Chron's disease and ulcerative colitis. The fusion protein retains the		
CC	ability to participate in well known immunological effector activities		
CC	including antibody dependent cell mediated cytotoxicity and/or complement		
CC	fixation in complement dependent cytotoxicity, despite having structures		
CC	that would not be expected to be capable of promoting the effector		
CC	activities. It can be produced in substantial quantities that are		
CC	typically greater than those routinely attained with single-chain		
CC	antibody constructs. This sequence encodes a chimeric fusion protein		
CC	created from the mouse anti-human CD20 single chain antibody variable		
CC	fragment (scFv) and the human extracellular domain short form CD154		
XX			
SQ	Sequence 1290 BP; 336 A; 324 C; 321 G; 309 T; 0 U; 0 Other;		
	Query Match	70.7%;	Score 483.4; DB 6; Length 1290;
	Best Local Similarity	99.8%;	Pred. No. 1.4e-133;
	Matches 484; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	200	CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC	259
Db	806	CTGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC	865
QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT	319
Db	866	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT	925
QY	320	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379
Db	926	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	985

QY	380	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439
Db	986	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	1045
QY	440	GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT	499
Db	1046	GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT	1105
QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT	559
Db	1106	TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT	1165
QY	560	TGGGAGGAGTATTTGAATTGCAATTCAAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	619
Db	1166	TGGGAGGAGTATTTGAATTGCAATTCAAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	1225
QY	620	GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT	679
Db	1226	GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT	1285
QY	680	CTAGA 684	
Db	1286	CTAGA 1290	
	RESULT 7		
	ADD25461		
ID	ADD25461	standard; DNA; 1290 BP.	
XX	AC	ADD25461;	
XX	DT	15-JAN-2004 (first entry)	
XX	DE	Binding domain-immunoglobulin fusion protein-associated DNA #12.	
XX	KW	ds; Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.	
OS	Unidentified.		
XX	PN	US2003118592-A1.	
XX	PD	26-JUN-2003.	
XX	PF	25-JUL-2002; 2002US-00207655.	
XX	PR	17-JAN-2001; 2001US-0367358P.	
PR	17-JAN-2002; 2002US-00053530.		
PR	03-JUN-2002; 2002US-0385691P.		
XX	PA	(GENE-) GENE-CRAFT INC.	
XX	PI	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;	
XX	DR	WPI; 2003-801317/75.	
XX	PT	New binding domain-immunoglobulin fusion protein, useful for treating a	
PT	subject having or suspected of having a malignant condition or a B-cell		
PT	disorder, e.g. melanoma, Grave's disease or autoimmune disease.		
XX	PS	Disclosure; SEQ ID NO 22; 157pp; English.	
XX	CC	Unidentified	
XX	SQ	Sequence 1290 BP; 336 A; 324 C; 321 G; 309 T; 0 U; 0 Other;	
	Query Match	70.7%;	Score 483.4; DB 10; Length 1290;

```
Best Local Similarity 99.8%; Pred. No. 1.4e-133;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
Db 806 CTGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 865

QY 260 ATGTCATAAGTGAGGCCAGCGAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
Db 866 ATGTCATAAGTGAGGCCAGCGAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 925

QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 926 ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 985

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 986 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1045

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCT 499
Db 1046 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCT 1105

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 1106 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1165

QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCATGTGACTGATCCAA 619
Db 1166 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCATGTGACTGATCCAA 1225

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 679
Db 1226 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 1285

QY 680 CTAGA 684
Db 1286 CTAGA 1290

RESULT 8
ADD25590
ID ADD25590 standard; DNA; 1290 BP.
XX
AC ADD25590;
XX
DT 15-JAN-2004 (first entry)
DE Binding domain-immunoglobulin fusion protein-associated DNA #79.
XX
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
PN
XX US2003118592-A1.
XX
PD 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
PF
XX 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENE-CRAFT INC.
XX
```

```
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 151; 157pp; English.
XX
CC Unidentified
XX
SQ Sequence 1290 BP; 335 A; 324 C; 322 G; 309 T; 0 U; 0 Other;

Query Match 70.7%; Score 483.4; DB 10; Length 1290;
Best Local Similarity 99.8%; Pred. No. 1.4e-133;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
Db 806 CTGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 865

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
Db 866 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 925

QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 926 ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 985

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 986 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1045

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCT 499
Db 1046 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAAATCT 1105

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 1106 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1165

QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCATGTGACTGATCCAA 619
Db 1166 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTGTCATGTGACTGATCCAA 1225

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 679
Db 1226 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 1285

QY 680 CTAGA 684
Db 1286 CTAGA 1290

RESULT 9
ADM42736
ID ADM42736 standard; cDNA; 1290 BP.
XX
AC ADM42736;
XX
XX 03-JUN-2004 (first entry)
DE 2H7scFv-CD154 S4, a binding domain-Ig fusion protein for CD20/40, cDNA.
XX
KW Mouse; ss; gene; antibody; single chain antibody; scFv;
KW binding domain-immunoglobulin fusion protein;
KW immunoglobulin hinge region; heavy chain CH2 constant region;
KW heavy chain CH3 constant region;
KW antibody dependent cell-mediated cytotoxicity; complement fixation; IgA;
KW IgG; CD19; CD20; CD37; CD40; L6; CD154; malignant condition; cancer;
KW B-cell disorder; autoantibody; rheumatoid arthritis; myasthenia gravis;
KW Grave's disease; type I diabetes mellitus; multiple sclerosis;
```

KW autoimmune disease; human.  
XX  
OS Mus musculus.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
PN US2003133939-A1.  
XX  
XX 17-JUL-2003.  
PD  
XX 17-JAN-2002; 2002US-00053530.  
PF  
XX 17-JAN-2002; 2002US-00053530.  
PR  
XX  
PA (GENE-) GENE-CRAFT INC.  
XX  
XX Ledbetter JA, Hayden-Ledbetter MS;  
PI  
XX WPI; 2003-843256/78.  
DR P-PSDB; ADM42748.  
DR  
XX  
PT New binding domain-immunoglobulin fusion protein for treating malignant  
PT conditions (e.g. cancer) or B-cell disorders, comprises a binding domain  
PT polypeptide and immunoglobulin heavy chain CH2 and CH3 constant region  
PT polypeptides.  
XX  
PS Example 4; SEQ ID NO 22; 80pp; English.  
XX  
XX The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC fusion protein is capable of at least one immunological activity such as  
CC antibody dependent cell-mediated cytotoxicity and complement fixation,  
CC and is capable of specifically binding to an antigen. The hinge region,  
CC polypeptide is selected from a mutated hinge region polypeptide that  
CC contains no cysteine residues (and that is derived from a wild-type  
CC immunoglobulin hinge region polypeptide having one or more cysteine  
CC residues), a mutated hinge region polypeptide that contains one cysteine  
CC residue (nd that is derived from a wild-type immunoglobulin hinge region  
CC polypeptide having two or more cysteine residues), a wild-type human  
CC immunoglobulin (Ig)A hinge region polypeptide, a mutated human IgA hinge  
CC region polypeptide that contains no cysteine residues (and that is  
CC derived from a wild-type human IgA region polypeptide) and a mutated  
CC human IgA hinge region polypeptide that contains one cysteine residue  
CC (and that is derived from a wild-type human IgA region polypeptide). Also  
CC included are an isolated polynucleotide encoding the novel fusion  
CC protein, a recombinant expression construct comprising the  
CC polynucleotide, a host cell transformed or transfected with the  
CC expression construct, producing the novel fusion protein (comprising  
CC culturing the host cell under conditions that permit expression of the  
CC novel fusion protein and isolating the binding domain-immunoglobulin  
CC fusion protein from the host cell culture), a pharmaceutical composition  
CC comprising the novel fusion protein in combination with a carrier and  
CC treating a subject having or suspected of having a malignant condition or  
CC a B-cell disorder (comprising administering to the patient an amount of  
CC the novel fusion protein). The mutated hinge region polypeptide exhibits  
CC a reduced ability to dimerise, relative to a wild-type human  
CC immunoglobulin G hinge region polypeptide. The binding domain polypeptide  
CC comprises at least one immunoglobulin variable region polypeptide  
CC selected from an immunoglobulin light chain variable region polypeptide  
CC and an immunoglobulin heavy chain variable region polypeptide, and  
CC optionally at least one linker peptide that is fused to the  
CC immunoglobulin variable region polypeptide. The immunoglobulin variable  
CC and constant region polypeptides are derived from a human immunoglobulin.  
CC The immunoglobulin heavy chain constant region CH2 and CH3 polypeptides  
CC are of an isotype selected from human IgG and human IgA. The antigen is  
CC selected from CD19, CD20, CD37, CD40 and L6. The binding domain  
CC polypeptide comprises a CD154 extracellular domain, and optionally, at  
CC least one immunoglobulin variable region polypeptide (e.g. mouse V1 and

CC Vh regions forming single chain antibodies which bind to one of the above  
CC antigens). The composition and methods are useful in treating malignant  
CC conditions (e.g. cancer) and B-cell disorders, including diseases  
CC characterised by autoantibody production, such as rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune diseases. The present sequence encodes a fusion  
CC protein of the invention comprising mouse antibody V1 and Vh regions  
CC fused to either human Immunoglobulin sequence or CD154 extracellular  
CC domain.

XX  
SQ Sequence 1290 BP; 336 A; 324 C; 321 G; 309 T; 0 U; 0 Other;

Query Match 70.7%; Score 483.4; DB 11; Length 1290;  
Best Local Similarity 99.8%; Pred. No. 1.4e-133;  
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC 259  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
806 CTGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC 865  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 319  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
866 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 925  
QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
926 ACTACACCATGAGCAACAACCTTGGTAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA 985  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
986 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1045  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTCT 499  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1046 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTCT 1105  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAAACCTTGCGGGCAACAATCCTCAATCACT 559  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1106 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAAACCTTGCGGGCAACAATCCTCAATCACT 1165  
QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAA 619  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1166 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAA 1225  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTTGGCTTACTCAAACCTCGAGTGATAAT 679  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1226 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTTGGCTTACTCAAACCTCGAGTGATAAT 1285  
QY 680 CTAGA 684  
Db |||||  
1286 CTAGA 1290

RESULT 10  
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ID AAF82932 standard; cDNA; 906 BP.  
XX  
AC AAF82932;  
XX  
DT 11-SEP-2003 (revised)  
DT 29-JUN-2001 (first entry)  
XX  
DE HIV-1 gp120 V3 loop-CD154 long form extracellular domain fusion cDNA.

XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;  
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;  
KW HIV-1; gp120; human; CD154; fusion protein; ss.  
XX Human immunodeficiency virus 1.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 13. .906



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FT misc_feature 73..198
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FT /note= "HIV-1 gp120 V3 loop coding sequence"
FT misc_feature 199..249
FT /note= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 250..906
FT /note= e
FT /note= "human CD154 long form extracellular domain coding
FT sequence"
XX
XX WO200126608-A2.
XX
XX 19-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028414.
XX
XX 14-OCT-1999; 99US-0159690P.
XX
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
XX
XX Ledbetter JA, Hayden-Ledbetter MS;
XX
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62337.
XX
XX DNA vaccine for improving antigen-specific humoral and cellular immune
XX responses, comprising one or more antigens linked to a domain that binds
XX at least one receptor.
XX
XX Example 1; Fig 2A; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked
XX to a domain that binds at least one receptor to improve the antigen-
XX specific humoral and cellular immune response. The DNA vaccines induce
XX strong antigen-specific humoral and cellular immune responses. The
XX vaccine can be use against acquired immunodeficiency syndrome (AIDS). The
XX present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
XX CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3
XX linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 906 BP; 294 A; 179 C; 216 G; 217 T; 0 U; 0 Other;
XX
XX Query Match 70.0%; Score 478.6; DB 4; Length 906;
XX Best Local Similarity 99.2%; Pred. No. 3.2e-132;
XX Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 200 CGGATCCAGAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
DB |||
DB 422 CGAAGAAAGAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 481
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
DB |||
DB 482 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 541
QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
DB |||
DB 542 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 601
QY 380 GACAAGGACTCTATTATATCTATGCCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
DB |||
DB 602 GACAAGGACTCTATTATATCTATGCCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 661
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499
DB |||
DB 662 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 721
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACT 559
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```
Db 722 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCGGGGCAACAATCCATTCACT 781
QY 560 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTCAATGTGACTGATCCAA 619
Db 782 TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTCAATGTGACTGATCCAA 841
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 679
Db 842 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 901
QY 680 CTAGA 684
Db 902 CTAGA 906
XX
XX RESULT 11
XX ABK89857
XX ID ABK89857 standard; DNA; 1470 BP.
XX
XX AC ABK89857;
XX
XX 05-NOV-2002 (first entry)
XX
XX Synthetic mouse/human chimeric fusion gene #5.
XX
XX Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
XX neuroprotective; gene therapy; single chain antibody; variable fragment;
XX scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
XX malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
XX Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
XX multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
XX immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
XX ulcerative colitis; inflammatory bowel disease; immunological effector;
XX cell mediated cytotoxicity; complement dependent cytotoxicity;
XX complement fixation; gene; ds; mouse; human.
XX
XX Mus musculus.
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
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XX Key Location/Qualifiers
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XX variable fragment (scFv)"
XX CDS 13..1461 /*tag= a
XX /product= "Mouse/human chimeric fusion protein"
XX misc_feature 814..1455 /*tag= c
XX /note= "Human extracellular domain long form CD154"
XX
XX WO200255910-A1.
XX
XX 25-JUL-2002.
XX
XX 17-JAN-2002; 2002WO-US001487.
XX
XX 17-JAN-2001; 2001US-00765208.
XX
XX (GENE-) GENE-CRAFT INC.
XX
XX Ledbetter JA, Hayden-Ledbetter M;
XX
XX WPI; 2002-599691/64.
XX P-PSDB; ABG31031.
XX
XX New human binding domain-immunoglobulin fusion protein useful for
XX treating a subject having or suspected of having a B-cell disorder or
XX malignant condition e.g. rheumatoid arthritis.
XX
```

PS Disclosure; Fig 7A-B; 136pp; English.

XX The invention describes a binding domain-immunoglobulin fusion protein that is capable of at least one immunological activity, comprising a binding domain polypeptide fused to an immunoglobulin hinge region polypeptide capable of specifically binding to an antigen, or an immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused to the hinge region polypeptide or to the CH2 constant region polypeptide. The fusion protein is useful for treating a subject having or suspected of having a B-cell disorder or malignant condition e.g. rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura, psoriasis, scleroderma, cancer and inflammatory bowel disease such as Chron's disease and ulcerative colitis. The fusion protein retains the ability to participate in well known immunological effector activities including antibody dependent cell mediated cytotoxicity and/or complement fixation in complement dependent cell mediated cytotoxicity and/or complement activities. It can be produced in substantial quantities that are typically greater than those routinely attained with single-chain antibody constructs. This sequence encodes a chimeric fusion protein created from the mouse anti-human CD20 single chain antibody variable fragment (scFv) and the human extracellular domain long form CD154

XX Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;

Query Match 70.0%; Score 478.6; DB 6; Length 1470;  
Best Local Similarity 99.2%; Pred. No. 3.9e-132;  
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259  
||| |||||||  
Db 986 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 1045

QY 260 ATGTCATAAGTGAGGCCAGCACTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319  
|||||  
Db 1046 ATGTCATAAGTGAGGCCAGCACTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 1105

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAAACAGCTGACCGTTAAAA 379  
|||||  
Db 1106 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAAACAGCTGACCGTTAAAA 1165

QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
|||||  
Db 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 1225

QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499  
|||||  
Db 1226 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 1285

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559  
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Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1345

QY 560 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAA 619  
|||||  
Db 1346 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAA 1405

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCTTGGCTTACTCAAACTCGAGTGATAAT 679  
|||||  
Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCACGTCTTGGCTTACTCAAACTCGAGTGATAAT 1465

QY 680 CTAGA 684  
|||||  
Db 1466 CTAGA 1470

RESULT 12  
ADD25460  
ID ADD25460 standard; DNA; 1470 BP.  
XX  
AC ADD25460;

XX 15-JAN-2004 (first entry)

DT Binding domain-immunoglobulin fusion protein-associated DNA #11.

XX ds; Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

OS US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

PF 17-JAN-2001; 2001US-0367358P.

XX 17-JAN-2002; 2002US-00053530.

PR 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENE-CRAFT INC.

PA Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 21; 157pp; English.

XX Unidentified

CC Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;

XX Query Match 70.0%; Score 478.6; DB 10; Length 1470;  
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QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
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QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499  
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Db 1226 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 1285

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559  
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Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1345

QY 560 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAA 619  
|||||  
Db 1346 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAA 1405







XX DNA vaccine for improving antigen-specific humoral and cellular immune  
PT responses, comprising one or more antigens linked to a domain that binds  
PT at least one receptor.  
XX  
PS Example 1; Fig 3A; 55pp; English.  
PS  
XX The invention provides a vaccine comprising one or more antigens linked  
CC to a domain that binds at least one receptor to improve the antigen-  
CC specific humoral and cellular immune response. The DNA vaccines induce  
CC strong antigen-specific humoral and cellular immune responses. The  
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The  
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154  
CC long form extracellular domain fusion protein linked by a ProAspPro  
CC linker. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;  
  
Query Match 70.0%; Score 478.6; DB 4; Length 2209;  
Best Local Similarity 99.2%; Pred. No. 4.6e-132;  
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGCGGCAC 259  
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1724 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGCGGCAC 1783  
  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1784 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 1843  
  
QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAA 379  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1844 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAAA 1903  
  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
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1904 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1963  
  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1964 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 2023  
  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAACAATCCATTCACT 559  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2024 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAACAATCCATTCACT 2083  
  
QY 560 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2084 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 2143  
  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 679  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2144 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTCGAGTGATAAT 2203  
  
QY 680 CTAGA 684  
Db |||||  
2204 CTAGA 2208

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	463.6	67.8	786	5 PCT-US93-10034-3	Sequence 3, Appli
3	463.6	67.8	840	1 US-07-940-605A-1	Sequence 1, Appli
4	463.6	67.8	840	1 US-08-184-422-7	Sequence 7, Appli
5	463.6	67.8	840	1 US-08-360-923A-1	Sequence 1, Appli
6	463.6	67.8	840	1 US-08-431-055-3	Sequence 3, Appli
7	463.6	67.8	840	2 US-08-690-096-1	Sequence 1, Appli
8	463.6	67.8	840	2 US-08-249-189-11	Sequence 11, Appl
9	463.6	67.8	840	2 US-08-484-624A-11	Sequence 11, Appl
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14	463.6	67.8	840	3 US-08-769-819-11	Sequence 11, Appl
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19	463.6	67.8	840	4 US-09-430-448-1	Sequence 1, Appli
20	463.6	67.8	879	4 US-09-645-926A-1	Sequence 1, Appli
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25	463.6	67.8	929	3 US-09-088-913A-20	Sequence 20, Appl
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28	463.6	67.8	929	3 US-08-770-981-20	Sequence 20, Appl
29	463.6	67.8	929	4 US-09-399-106-20	Sequence 20, Appl
30	463.6	67.8	1425	2 US-08-249-189-15	Sequence 15, Appl
31	463.6	67.8	1425	2 US-08-484-624A-15	Sequence 15, Appl
32	463.6	67.8	1425	2 US-08-477-733B-15	Sequence 15, Appl
33	463.6	67.8	1425	3 US-09-088-913A-15	Sequence 15, Appl
34	463.6	67.8	1425	3 US-08-769-819-15	Sequence 15, Appl
35	463.6	67.8	1425	3 US-08-770-974-15	Sequence 15, Appl
36	463.6	67.8	1425	3 US-08-770-981-15	Sequence 15, Appl
37	463.6	67.8	1425	4 US-09-399-106-15	Sequence 15, Appl
38	463.6	67.8	1803	4 US-09-909-595-3	Sequence 3, Appli
39	463.6	67.8	1816	4 US-09-645-926A-5	Sequence 5, Appli
40	448.4	65.6	839	4 US-09-023-655-919	Sequence 919, App
41	366.4	53.6	633	4 US-09-322-409-77	Sequence 77, Appl
C 42	366.4	53.6	633	4 US-09-322-409-79	Sequence 79, Appl
43	366.4	53.6	633	4 US-09-451-527-77	Sequence 77, Appl
C 44	366.4	53.6	633	4 US-09-451-527-79	Sequence 79, Appl
45	366.4	53.6	780	4 US-09-322-409-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1  
US-08-446-922-3  
; Sequence 3, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 786 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; STRAIN: CD40-L  
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..783
US-08-446-922-3

Query Match          67.8%; Score 463.6; DB 1; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.3e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAATTCGGGCAC 259
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Db 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAATTCGGGCAC 373

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
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Db 374 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 433

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
   |||
Db 434 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 493

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA 439
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Db 494 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA 553

QY 440 GTCGAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
   |||
Db 554 GTCGAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 613

QY 500 TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTGGGGAACAAATCCATTCACT 559
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Db 614 TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTGGGGAACAAATCCATTCACT 673

QY 560 TGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
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Db 674 TGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 669
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Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 783
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RESULT 2
PCT-US93-10034-3
; Sequence 3, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
PCT-US93-10034-3

Query Match          67.8%; Score 463.6; DB 5; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.3e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAATTCGGGCAC 259
   |||
Db 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAATTCGGGCAC 373

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
   |||
Db 374 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 433

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
   |||
Db 434 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 493

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA 439
   |||
Db 494 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA 553

QY 440 GTCGAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
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Db 554 GTCGAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 613

QY 500 TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTGGGGAACAAATCCATTCACT 559
   |||
Db 614 TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTGGGGAACAAATCCATTCACT 673

QY 560 TGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
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Db 674 TGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 669
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Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACCTC 783

RESULT 3
US-07-940-605A-1
; Sequence 1, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,605A  
; FILING DATE: 04-SEP-1992  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 22..807  
; US-07-940-605A-1

Query Match 67.8%; Score 463.6; DB 1; Length 840;  
Best Local Similarity 99.1%; Pred. No. 1.4e-137;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTTGGGCAC 259  
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Db 335 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTTGGGCAC 394  
  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 319  
||| |||||  
Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 454  
  
QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATGGGAAACAGCTGACCGTTAAAA 379  
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Db 455 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATGGGAAACAGCTGACCGTTAAAA 514  
  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
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Db 515 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 574  
  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499  
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Db 575 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 634  
  
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QY 560 TGGGAGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA 619  
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Db 695 TGGGAGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA 754  
  
QY 620 GCCAAGTGAGCCATGGCCTGCTTACGCTCCTTTGGCTTACTCAAACCTC 669  
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Db 755 GCCAAGTGAGCCATGGCCTTACGCTCCTTTGGCTTACTCAAACCTC 804

RESULT 4  
US-08-184-422-7  
; Sequence 7, Application US/08184422  
; Patent No. 5565321  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: RENSHAW, BLAIR

;  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: WIDMER, MICHAEL  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
; TITLE OF INVENTION: IN A CD40 LIGAND GENE  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: MS Word for Apple 5.1, Version a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/184,422  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/009,258  
; FILING DATE: 01/22/93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERKINS, PATRICIA ANNE  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2810-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
; US-08-184-422-7

Query Match 67.8%; Score 463.6; DB 1; Length 840;  
Best Local Similarity 99.1%; Pred. No. 1.4e-137;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTTGGGCAC 259  
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Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTTGGGCAC 418  
  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 319  
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Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 478  
  
QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAA 379  
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Db 479 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAAACAGCTGACCGTTAAAA 538  
  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
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Db 539 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 598  
  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499  
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Db 599 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 658



QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTGCGGGCAACAATCCATTCACT	559
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QY	560	TGGGAGGAGTATTTGAATTGC AAC CAGGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAA	619
Db	719	TGGGAGGAGTATTTGAATTGC AAC CAGGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAA	778
QY	620	GCCAAGTGAGCCATGGC ACTGGCTTCACGTCTCTTTGGCTTACTCAAATC	669
Db	779	GCCAAGTGAGCCATGGC ACTGGCTTCACGTCTCTTTGGCTTACTCAAATC	828

## RESULT 5

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US-08-360-923A-1
; Sequence 1, Application US/08360923A
; Patent No. 5674492
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: LONGO, DAN L.
; APPLICANT: MURPHY, WILLIAM
; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
; TITLE OF INVENTION: EXPRESSING CD40
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,923A
; FILING DATE: December 21, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/172,664
; FILING DATE: December 23, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2818-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
;
US-08-360-923A-1

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Matches	466;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QY	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC	259						
Db	359	CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC	418						
QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAAGGAT	319						
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAAGGAT	478						
QY	320	ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379						
Db	479	ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	538						
QY	380	GACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439						
Db	539	GACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	598						
QY	440	GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCT	499						
Db	599	GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCT	658						
QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTGGGGCAACAATCCATTCACT	559						
Db	659	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAAACCTTGGGGCAACAATCCATTCACT	718						
QY	560	TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	619						
Db	719	TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	778						
QY	620	GCCAAAGTGAGCCATGGCACTGGCTTCAAGTCTTTGGCTTACTCAAACTC	669						
Db	779	GCCAAAGTGAGCATGGCACTGGCTTCAAGTCTTTGGCTTACTCAAACTC	828						

## RESULT 6

US-08-431-055-3  
; Sequence 3, Application US/08431055  
; Patent No. 5817516  
; GENERAL INFORMATION:  
; APPLICANT: KEHRY, MERILYN R  
; APPLICANT: CASTLE, BRIAN E  
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 100 NEW YORK AVE. N.W. SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,055  
; FILING DATE: 28-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/234,580  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
US-08-431-055-3

Query Match          67.8%; Score 463.6; DB 1; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
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Db 335 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 394

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
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Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 454

QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
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Db 455 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 514

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439
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Db 515 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 574

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499
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QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGGGCAACAATCCATTCACT 559
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Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGGGCAACAATCCATTCACT 694

QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
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Db 695 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 754

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
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Db 755 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 804

RESULT 7
US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
US-08-690-096-1

Query Match          67.8%; Score 463.6; DB 2; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 335 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 394

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 454

QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 514

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 515 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 574

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 575 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 634

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGGGCAACAATCCATTCACT 559
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGGGCAACAATCCATTCACT 694

QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 695 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 754

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 755 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 804

RESULT 8
US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
;

```

STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,189  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-249-189-11

Query Match 67.8%; Score 463.6; DB 2; Length 840;  
Best Local Similarity 99.1%; Pred. No. 1.4e-137;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGCGGCAC 259  
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGCGGCAC 418  
QY 260 ATGTCATAAGTAGGCCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
419 ATGTCATAAGTAGGCCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478  
QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
479 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
539 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598  
QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAATCT 499  
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Db 599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAATCT 658  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGGGCAACAATCCATTCACT 559  
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Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619  
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 719 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 669  
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAAACTC 828  
RESULT 9  
US-08-484-624A-11  
; Sequence 11, Application US/08484624A  
; Patent No. 5962406  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,624A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single





Db 659 TACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGTAATTGCAACACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619  
Db 719 TGGGAGGAGTATTGTAATTGCAACACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 828  
RESULT 11  
US-08-763-995-1  
; Sequence 1, Application US/08763995  
; Patent No. 6017527  
; GENERAL INFORMATION:  
; APPLICANT: MARASKOVSKY, EUGENE  
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Power Macintosh 7200/90  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/763,995  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/677,762  
; FILING DATE: 10 JUL 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2845-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
US-08-763-995-1  
Query Match 67.8%; Score 463.6; DB 3; Length 840;  
Best Local Similarity 99.1%; Pred. No. 1.4e-137;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC 259  
Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCAC 418

QY 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db 419 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478  
QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAACCTGGGAAATGGGAAACAGCTGACCGTTAAAA 379  
Db 479 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAACCTGGGAAATGGGAAACAGCTGACCGTTAAAA 538  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
Db 539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499  
Db 599 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 658  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559  
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGTAATTGCAACACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619  
Db 719 TGGGAGGAGTATTGTAATTGCAACACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 828  
RESULT 12  
US-09-088-913A-11  
; Sequence 11, Application US/09088913A  
; Patent No. 6087329  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,913A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-088-913A-11

	Query Match	67.8%;	Score 463.6;	DB 3;	Length 840;
	Best Local Similarity	99.1%;	Pred. No. 1.4e-137;		
	Matches 466;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	259		
Db	359	CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	418		
Qy	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	478		
Qy	320	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGAAAAACAGCTGACCCGTTAAAA	379		
Db	479	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGAAAAACAGCTGACCCGTTAAAA	538		
Qy	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCGTTCCTTCCAATCGGGAAGCTTCGA	439		
Db	539	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCGTTCCTTCCAATCGGGAAGCTTCGA	598		
Qy	440	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCT	499		
Db	599	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCT	658		
Qy	500	TACTCAGAGCTGCAATATACCCACAGTTCGCGCCAAACCTTTGGGGCAACAATCCATTCACT	559		
Db	659	TACTCAGAGCTGCAATATACCCACAGTTCGCGCCAAACCTTTGGGGCAACAATCCATTCACT	718		
Qy	560	TGGGAGGAGTATTTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	619		
Db	719	TGGGAGGAGTATTTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	778		
Qy	620	GCCAAGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC	669		
Db	779	GCCNAGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACCTC	828		

RESULT 13  
US-08-589-771B-7  
; Sequence 7, Application US/08589771B  
; Patent No. 6106832  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: RENSRAW, BLAIR  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: WIDMER, MICHAEL

```

; TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
; TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,771B
; FILING DATE: January 22, 1996
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/009,258
; FILING DATE: 01/22/93
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY, JANIS C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2810-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
;
; US-08-589-771B-7

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	Query Match	67.8%;	Score 463.6;	DB 3;	Length 840;
	Best Local Similarity	99.1%;	Pred. NO. 1.4e-137;		
	Matches 466;	Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;
QY	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC	259		
Db	359	CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC	418		
QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	478		
QY	320	ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379		
Db	479	ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA	538		
QY	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439		
Db	539	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	598		
QY	440	GTCAAGCTCCATTTATAGCCAGCCTCTGCCATAAGTCCCCCGGTAGATTCGAGAGAATCT	499		
Db	599	GTCAAGCTCCATTTATAGCCAGCCTCTGCCATAAGTCCCCCGGTAGATTCGAGAGAATCT	658		
QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGCGGGCAACAATCCATTCACT	559		



Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619  
Db 719 TGGGAGGAGTATTGAAATTGCAACCAAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 828

RESULT 14

US-08-769-819-11  
; Sequence 11, Application US/08769819  
; Patent No. 6264951  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,819  
; FILING DATE: 19-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: 08/249,189  
; FILING DATE: May 24, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:

; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
US-08-769-819-11  
Query Match 67.8%; Score 463.6; DB 3; Length 840;  
Best Local Similarity 99.1%; Pred. No. 1.4e-137;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 259  
Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC 418  
QY 260 ATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319  
Db 419 ATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 478  
QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCCTGGAATAATGGGAAACAGCTGACCGTTAAAA 379  
Db 479 ACTACACCATGAGCAACAACCTTGGTAAACCCTGGAATAATGGGAAACAGCTGACCGTTAAAA 538  
QY 380 GACAAGGACTCTATTATATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTGA 439  
Db 539 GACAAGGACTCTATTATATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTGA 598  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499  
Db 599 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 658  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCCGCCAAACCTTGGGGCAACAATCCATTCACT 559  
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCCCGCCAAACCTTGGGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619  
Db 719 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 828

RESULT 15

US-08-770-974-11  
; Sequence 11, Application US/08770974  
; Patent No. 6290972  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,974  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733

; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-770-974-11

Search completed: November 12, 2004, 12:57:46
Job time : 41.1199 secs

Query Match		67.8%;	Score 463.6;	DB 3;	Length 840;
Best Local Similarity		99.1%;	Pred. No. 1.4e-137;		
Matches	466;	Conservative	0;	Mismatches	4;
				Indels	0;
				Gaps	0;
Qy	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	259		
Db	359	CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	418		
Qy	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	478		
Qy	320	ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGGAAACAGCTGACCCGTTAAAA	379		
Db	479	ACTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGGAAACAGCTGACCCGTTAAAA	538		
Qy	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439		
Db	539	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	598		
Qy	440	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTCT	499		
Db	599	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTCT	658		
Qy	500	TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT	559		
Db	659	TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACT	718		
Qy	560	TGGGAGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAA	619		
Db	719	TGGGAGGAGTATTGGAATTGCAACCAAGTGTCTCGGTGTTGTCAATGTGACTGATCCAA	778		
Qy	620	GCCAAGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC	669		
Db	779	GCCAAGTGAGCCATGGCAGTGGCTTCACGTCTCTTTGGCTTACTCAAACTC	828		

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Db 806 CTGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 865  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db 866 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 925  
QY 320 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db 926 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 985  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
Db 986 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1045  
QY 440 GTCGAAGCTCCATTTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499  
Db 1046 GTCGAAGCTCCATTTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1105  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCAGGCAACAATCCATTCACT 559  
Db 1106 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCAGGCAACAATCCATTCACT 1165  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619  
Db 1166 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 1225  
QY 620 GCCAAGTGAGCCATGGCCTTCACGTCTTTGGCTTACTCAAACTCGAGTGATAAT 679  
Db 1226 GCCAAGTGAGCCATGGCCTTCACGTCTTTGGCTTACTCAAACTCGAGTGATAAT 1285  
QY 680 CTAGA 684  
Db 1286 CTAGA 1290

RESULT 2

US-10-207-655-151  
; Sequence 151, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 151  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mouse-Human hybrid fusion protein  
US-10-207-655-151

Query Match 70.7%; Score 483.4; DB 15; Length 1290;  
Best Local Similarity 99.8%; Pred. No. 1.2e-134;  
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259  
Db 806 CTGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 865  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db 866 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 925  
QY 320 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db 926 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 985  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439

Db 986 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1045  
QY 440 GTCGAAGCTCCATTTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499  
Db 1046 GTCGAAGCTCCATTTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 1105  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCAGGCAACAATCCATTCACT 559  
Db 1106 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCAGGCAACAATCCATTCACT 1165  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619  
Db 1166 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 1225  
QY 620 GCCAAGTGAGCCATGGCCTTCACGTCTTTGGCTTACTCAAACTCGAGTGATAAT 679  
Db 1226 GCCAAGTGAGCCATGGCCTTCACGTCTTTGGCTTACTCAAACTCGAGTGATAAT 1285  
QY 680 CTAGA 684  
Db 1286 CTAGA 1290

RESULT 3

US-10-053-530-22  
; Sequence 22, Application US/10053530  
; Publication No. US20030133939A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey  
; APPLICANT: Hayden-Ledbetter, Martha  
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 390069.401  
; CURRENT APPLICATION NUMBER: US/10/053,530  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 09/765,208  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MOUSE-HUMAN HYBRID  
; NAME/KEY: misc feature  
; LOCATION: (13)..(808)  
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV  
; NAME/KEY: misc feature  
; LOCATION: (814)..(1275)  
; OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154  
US-10-053-530-22

Query Match 70.7%; Score 483.4; DB 15; Length 1290;  
Best Local Similarity 99.8%; Pred. No. 1.2e-134;  
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259  
Db 806 CTGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 865  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db 866 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 925  
QY 320 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
Db 926 ACTACACCATGAGCAACAACACTTGGTAAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA 985  
QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
Db 986 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1045

QY	440	GTCAAGCTCCATTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT	499
Db	1046	GTCAAGCTCCATTATAGCAGCCTCTGCCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT	1105
QY	500	TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTCGGGCAACAATCCATTCACT	559
Db	1106	TACTCAGAGCTGCAATATACCCACAGTTCGCCCAACCTTCGGGCAACAATCCATTCACT	1165
QY	560	TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTCTGTCAATGTGACTGATCCAA	619
Db	1166	TGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTCTGTCAATGTGACTGATCCAA	1225
QY	620	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACCTCGAGTGATAAT	679
Db	1226	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACCTCGAGTGATAAT	1285
QY	680	CTAGA	684
Db	1286	CTAGA	1290

## RESULT 4

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US-10-207-655-21
; Sequence 21, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MOUSE-HUMAN HYBRID
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(808)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (814)..(1455)
; OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154
US-10-207-655-21

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Query Match	70.0%;	Score 478.6;	DB 15;	Length 1470;
Best Local Similarity	99.2%;	Pred. No. 3.4e-133;		
Matches 481;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	200	CGGATCCAGAAAAACAGCTTTGAAAATGCAAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC	259	
Db	986	CGAAGAAAGAAAAACAGCTTTGAAAATGCAAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC	1045	
QY	260	ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTCTGTTACAGTGGGCTGAAAAAGGAT	319	
Db	1046	ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTCTGTTACAGTGGGCTGAAAAAGGAT	1105	
QY	320	ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGAAACAGCTGACCGTTAAAA	379	
Db	1106	ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAAAATGGAAACAGCTGACCGTTAAAA	1165	
QY	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGA	439	
Db	1166	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGA	1225	
QY	440	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT	499	
Db	1226	GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT	1285	

QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT	559
Db	1286	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT	1345
QY	560	TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	619
Db	1346	TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA	1405
QY	620	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT	679
Db	1406	GCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT	1465
QY	680	CTAGA	684
Db	1466	CTAGA	1470

## RESULT 5

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US-10-207-655-149
; Sequence 149, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse-Human hybrid fusion protein
US-10-207-655-149

```

	Query Match	70.0%;	Score 478.6;	DB 15;	Length 1470;
	Best Local Similarity	99.2%;	Pred. No. 3.4e-133;		
	Matches 481;	Conservative	0;	Mismatches 4;	Indels 0;
					Gaps 0;
QY	200	CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	259		
DB	986	CGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAATTCGGGCAC	1045		
QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
DB	1046	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	1105		
QY	320	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA	379		
DB	1106	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAA	1165		
QY	380	GACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439		
DB	1166	GACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	1225		
QY	440	GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAATCT	499		
DB	1226	GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAATCT	1285		
QY	500	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGCGGGCAACAATCCATTCACT	559		
DB	1286	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTGGCGGGCAACAATCCATTCACT	1345		
QY	560	TGGGAGGAGTATTTGAATTGCAACCCAGGTGTTTCGGTGTGTTGTCAATGTGACTGATCCAA	619		
DB	1346	TGGGAGGAGTATTTGAATTGCAACCCAGGTGTTTCGGTGTGTTGTCAATGTGACTGATCCAA	1405		
QY	620	GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT	679		



Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTCGAGTGATAAT 1465

QY 680 CTAGA 684

Db 1466 CTAGA 1470

RESULT 6

US-10-053-530-21

; Sequence 21, Application US/10053530

; Publication No. US20030133939A1

; GENERAL INFORMATION:

; APPLICANT: Ledbetter, Jeffrey

; APPLICANT: Hayden-Ledbetter, Martha

; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins

; FILE REFERENCE: 390069.401

; CURRENT APPLICATION NUMBER: US/10/053,530

; CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: US 09/765,208

; PRIOR FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 21

; LENGTH: 1470

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: MOUSE-HUMAN HYBRID

; NAME/KEY: misc\_feature

; LOCATION: (1)-(808)

; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV

; NAME/KEY: misc\_feature

; LOCATION: (814)-(1455)

; OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

US-10-053-530-21

Query Match 70.0%; Score 478.6; DB 15; Length 1470;

Best Local Similarity 99.2%; Pred. No. 3.4e-133;

Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259

Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 1045

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319

Db 1046 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 1105

QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTTGAAATGGGAAACAGCTGACCGTTAAAA 379

Db 1106 ACTACACCATGAGCAACAACCTTGGTAAACCTTGAAATGGGAAACAGCTGACCGTTAAAA 1165

QY 380 GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAGCTTCGA 439

Db 1166 GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAGCTTCGA 1225

QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 499

Db 1226 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 1285

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559

Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 1345

QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619

Db 1346 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 1405

QY 620 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAACCTCGAGTGATAAT 679

Db 1406 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAACCTCGAGTGATAAT 1465

QY 680 CTAGA 684

Db 1466 CTAGA 1470

RESULT 7

US-10-312-245-6

; Sequence 6, Application US/10312245

; Publication No. US20030219419A1

; GENERAL INFORMATION:

; APPLICANT: University of Louisville Research Foundation, Inc.

; APPLICANT: Shirwan, Haval

; TITLE OF INVENTION: Methods and Compositions for Altering Cell Membrane Function.

; FILE REFERENCE: 1160.015WO1

; CURRENT APPLICATION NUMBER: US/10/312,245

; CURRENT FILING DATE: 2002-12-23

; PRIOR APPLICATION NUMBER: US 60/215,580

; PRIOR FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 1566

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SA-CD40L

US-10-312-245-6

Query Match 68.1%; Score 466; DB 15; Length 1566;

Best Local Similarity 98.9%; Pred. No. 2.2e-129;

Matches 469; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 259

Db 766 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGGGCAC 825

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319

Db 826 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 885

QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTTGAAATGGGAAACAGCTGACCGTTAAAA 379

Db 886 ACTACACCATGAGCAACAACCTTGGTAAACCTTGAAATGGGAAACAGCTGACCGTTAAAA 945

QY 380 GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAGCTTCGA 439

Db 946 GACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTTCCAATCGGGAAGCTTCGA 1005

QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 499

Db 1006 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 1065

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559

Db 1066 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 1125

QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619

Db 1126 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 1185

QY 620 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAACCTCGAGT 673

Db 1186 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCCTTTGGCTTACTCAAACCTCGAAT 1239

RESULT 8

US-09-365-940-11

; Sequence 11, Application US/09365940

; Publication No. US20030091564A1

; GENERAL INFORMATION:

; APPLICANT: ARMITAGE, RICHARD

; APPLICANT: FANSLAW, WILLIAM

; APPLICANT: SPRIGGS, MELANIE

; APPLICANT: SRINIVASAN, SUBHASHINI



APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,940  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-365-940-11

Query Match 67.8%; Score 463.6; DB 10; Length 840;  
Best Local Similarity 99.1%; Pred. No. 8.5e-129;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTGGGCAC 259  
Db 359 CGAAGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTGGGCAC 418  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319  
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478

QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAATGCGAAACACAGCTGACCGTTAAAA 379  
Db 479 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAAATGCGAAACACAGCTGACCGTTAAAA 538  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439  
Db 539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598  
QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 499  
Db 599 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCT 658  
QY 500 TACTCAGAGCTGCAATATACCCACAGTTCGCGCAAACTTTCGCGGCAACAATCCATTCACT 559  
Db 659 TACTCAGAGCTGCAATATACCCACAGTTCGCGCAAACTTTCGCGGCAACAATCCATTCACT 718  
QY 560 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619  
Db 719 TGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGCTTACTCAAACTC 669  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGCTTACTCAAACTC 828

RESULT 9  
US-10-294-176-1  
; Sequence 1, Application US/10294176  
; Publication No. US20030077263A1  
; GENERAL INFORMATION:  
; APPLICANT: MARASKOVSKY, EUGENE  
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Power Macintosh 7200/90  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/294,176  
; FILING DATE: 14-No. US20030077263A1-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/430,448  
; FILING DATE: 29-Oct-1999  
; APPLICATION NUMBER: 08/763,995  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2845-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens

```

; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-294-176-1

Query Match      67.8%; Score 463.6; DB 14; Length 840;
Best Local Similarity 99.1%; Pred. No. 8.5e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259
Db 359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 418

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAANAATGGGAAAACAGCTGACCGTTAAAA 379
Db 479 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAANAATGGGAAAACAGCTGACCGTTAAAA 538

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGGAAGCTTCGA 439
Db 539 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGGAAGCTTCGA 598

QY 440 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCT 499
Db 599 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCT 658

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCCGCGGCAACAATCCATTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCCGCGGCAACAATCCATTCACT 718

QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db 719 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 828

RESULT 10
US-10-200-242-11
; Sequence 11, Application US/10200242
; Publication No. US2003014182A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLOW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11
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; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11

Query Match      67.8%; Score 463.6; DB 15; Length 840;
Best Local Similarity 99.1%; Pred. No. 8.5e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259
Db 359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 418

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAANAATGGGAAAACAGCTGACCGTTAAAA 379
Db 479 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAANAATGGGAAAACAGCTGACCGTTAAAA 538

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGGAAGCTTCGA 439
Db 539 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGGAAGCTTCGA 598

QY 440 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCT 499
Db 599 GTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTTCGAGAGAAATCT 658

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCCGCGGCAACAATCCATTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCCGCGGCAACAATCCATTCACT 718

QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db 719 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 778

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 828

RESULT 11
US-10-200-242-11
; Sequence 11, Application US/10200242
; Publication No. US20040006006A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLOW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11
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Query Match 67.8%; Score 463.6; DB 16; Length 840;  
Best Local Similarity 99.1%; Pred. No. 8.5e-129;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259  
|||  
Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 418  
|||  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319  
|||  
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGAT 478  
|||  
QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
|||  
Db 479 ACTACACCATGAGCAACAACCTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 538  
|||  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAGTCCCTTCAAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
|||  
Db 539 GACAAGGACTCTATTATATCTATGCCCCAGTCCCTTCAAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGA 598  
|||  
QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 499  
|||  
Db 599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 658  
|||  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAATCCATTCACT 559  
|||  
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAATCCATTCACT 718  
|||  
QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTGTTGTCGAATGTGACTGATCCAA 619  
|||  
Db 719 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTGTTGTCGAATGTGACTGATCCAA 778  
|||  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
|||  
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 828  
|||

RESULT 12  
US-10-242-212-1  
; Sequence 1, Application US/10242212  
; Publication No. US20030099644A1  
; GENERAL INFORMATION:  
; APPLICANT: AHUJA, SEEMA  
; APPLICANT: BONEWALD, LYNDA  
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 4003.001000  
; CURRENT APPLICATION NUMBER: US/10/242,212  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US/09/645,926  
; PRIOR FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 879  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-212-1

Query Match 67.8%; Score 463.6; DB 14; Length 879;  
Best Local Similarity 99.1%; Pred. No. 8.7e-129;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259  
|||  
Db 335 CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 394  
|||  
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319  
|||  
Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAAGGAT 454  
|||  
QY 320 ACTACACCATGAGCAACAACCTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379  
|||

Db 455 ACTACACCATGAGCAACAACCTTGGTAAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 514  
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439  
|||  
Db 515 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 574  
|||  
QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 499  
|||  
Db 575 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 634  
|||  
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAATCCATTCACT 559  
|||  
Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAATCCATTCACT 694  
|||  
QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTGTTGTCGAATGTGACTGATCCAA 619  
|||  
Db 695 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTGTTGTCGAATGTGACTGATCCAA 754  
|||  
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 669  
|||  
Db 755 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCCTTTGGCTTACTCAAACTC 804  
|||

RESULT 13  
US-09-365-940-20  
; Sequence 20, Application US/09365940  
; Publication No. US20030091564A1  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/365,940  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Human CD40-L trimer
; FEATURE:
; NAME/KEY: sig\_peptide
; LOCATION: 65..142
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 65..886
; FEATURE:
; NAME/KEY: mat\_peptide
; LOCATION: 143..886
;
US-09-365-940-20

Query Match 67.8%; Score 463.6; DB 10; Length 929;
Best Local Similarity 99.1%; Pred. No. 9e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
|||
Db 414 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 473

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
|||||
Db 474 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 533

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
|||||
Db 534 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 593

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
|||||
Db 594 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 653

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 499
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Db 654 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 713

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCGGGGCAACAATCCATTCACT 559
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QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
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Db 774 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 833

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACCTC 669
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Db 834 GCCAAGTGAGCCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACCTC 883

RESULT 14
US-10-200-242-20
; Sequence 20, Application US/10200242
; Publication No. US2003014182A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940

; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (65)..(883)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat\_peptide
; LOCATION: (143)..()
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig\_peptide
; LOCATION: (65)..(142)
; OTHER INFORMATION:
;
US-10-200-242-20

Query Match 67.8%; Score 463.6; DB 15; Length 929;
Best Local Similarity 99.1%; Pred. No. 9e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
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Db 414 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 473

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
|||||
Db 474 ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT 533

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
|||||
Db 534 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 593

QY 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
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Db 594 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 653

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 499
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Db 654 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 713

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCGGGGCAACAATCCATTCACT 559
|||||
Db 714 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCGGGGCAACAATCCATTCACT 773

QY 560 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 619
|||||
Db 774 TGGGAGGAGTATTGTAATTGCAACCAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCAA 833

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACCTC 669
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Db 834 GCCAAGTGAGCCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACCTC 883

RESULT 15
US-10-200-242-20
; Sequence 20, Application US/10200242
; Publication No. US20040006006A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION



; FILE REFERENCE: 2802-N  
; CURRENT APPLICATION NUMBER: US/10/200,242  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 09/365,940  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 08/769,819  
; PRIOR FILING DATE: 1996-12-19  
; PRIOR APPLICATION NUMBER: 08/484,624  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/249,189  
; PRIOR FILING DATE: 1994-05-24  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 929  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (65)..(883)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (143)..()  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (65)..(142)  
; OTHER INFORMATION:  
US-10-200-242-20

Query Match		67.8%;	Score 463.6;	DB 16;	Length 929;
Best Local Similarity		99.1%;	Pred. No. 9e-129;		
Matches	466;	Conservative	0;	Mismatches	4;
				Indels	0;
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Qy	320	ACTACACCATGAGCAACAACTTTGGTAAACCTGGAAATGGGAAACAGCTGACCGTTAAAAA	379		
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Qy	440	GTCAAGCTCCATTATTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTTCGAGAGAACTCT	499		
Db	654	GTCAAGCTCCATTATTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTTCGAGAGAACTCT	713		
Qy	500	TACTCAGAGCTGCAAAATACCCAGATTCCGCCAAACCTTCGGGGCAACAATCCATTCACT	559		
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Qy	560	TGGGAGGAGTATTGTAATGCAACAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA	619		
Db	774	TGGGAGGAGTATTGTAATGCAACAGGTGCTTCGGTGTGTGTCAATGTGACTGATCCAA	833		
Qy	620	GCCAAGTGAGCCATGGCATTACAGTCCCTTTGGCTTACTCAAACTC	669		
Db	834	GCCAAGTGAGCCATGGCATTACAGTCCCTTTGGCTTACTCAAACTC	883		

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:05:05 ; Search time 1501.63 Seconds  
(without alignments)  
16598.440 Million cell updates/sec

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Perfect score: 684  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463.6	67.8	786	9 AY416061	AY416061 Homo sapi
2	463.6	67.8	786	9 AY416062	AY416062 Pan trogl
3	390.8	57.1	767	6 CD638712	CD638712 AGENCOURT
4	330.2	48.3	783	9 AY416063	AY416063 Mus muscu
5	325.8	47.6	806	6 CD521613	CD521613 AGENCOURT
6	286.4	41.9	571	7 CN794193	CN794193 4129335 B
7	240	35.1	628	7 CN786611	CN786611 4120632 B
8	220.2	32.2	702	6 CD640741	CD640741 AGENCOURT
9	216	31.6	690	6 CD642064	CD642064 AGENCOURT
10	209.8	30.7	796	6 CD520208	CD520208 AGENCOURT
11	108.4	15.8	847	7 CK777858	CK777858 965004 MA
12	98.6	14.4	740	7 CK834247	CK834247 4058618 B
13	96.6	14.1	492	2 BF599437	BF599437 263218 MA
14	78.6	11.5	727	5 BU294618	BU294618 603603621
15	78.6	11.5	731	5 BU373331	BU373331 603589056
16	71.4	10.4	638	1 AI982044	AI982044 pat.pk007
17	59.6	8.7	268	6 CD727599	CD727599 4032503 1
18	58	8.5	803	5 BU398104	BU398104 603535227
19	46.6	6.8	878	9 CNS0187R	ALL08993 Drosophil
20	46	6.7	389	6 CA432817	CA432817 UI-H-COO-
21	46	6.7	997	9 CNS005TE	AL060767 Drosophil
22	45.2	6.6	1286	9 AG280276	AG280276 Mus muscu
23	44.2	6.5	861	5 BX367066	BX367066 BX367066
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C 25	43.6	6.4	1247	9	AG278972	Mus muscu
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28	42.6	6.2	1135	8	CC233138	CH261-192
29	42.2	6.2	507	9	CNS01852	Drosophil
30	41.8	6.1	787	9	CNS007XT	AL050971 Drosophil
C 31	41.8	6.1	982	9	CNS06JLK	AL401742 T7 end of
32	41.8	6.1	1076	9	CNS026ZE	AL184019 Tetraodon
C 33	41.8	6.1	1225	9	AG311152	AG311152 Mus muscu
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35	41.4	6.1	900	8	BH159228	BH159228 ENTRY51TR
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C 41	41.2	6.0	1182	9	CL019530	CL019530 CH216-5H1
C 42	41.2	6.0	1373	9	AG347201	AG347201 Mus muscu
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ALIGNMENTS

RESULT 1  
AY416061  
LOCUS  
DEFINITION -Homo sapiens TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY416061  
VERSION  
AY416061.1 GI:39772021  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 786)  
AUTHORS  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL  
Science 302 (5652), 1960-1963 (2003)  
PUBMED  
14671302  
REFERENCE  
2 (bases 1 to 786)  
AUTHORS  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
Location/Qualifiers  
source  
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ORIGIN  
Query Match 67.8%; Score 463.6; DB 9; Length 786;  
Best Local Similarity 99.1%; Pred. No. 2.2e-126;  
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 200 CGGATCCAGAAAACAGCTTTGAATGCAAAAGGTGATCAGAATCCTCAATTCGGCAC 259  
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Db 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 373

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QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439

Db 494 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 553

QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499

Db 554 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 613

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT 559

Db 614 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT 673

QY 560 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619

Db 674 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAATC 669

Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAATC 783

RESULT 2

AY416062

LOCUS

DEFINITION Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY416062

VERSION AY416062.1 GI:39772022

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 786)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 786)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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source

1. .786

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

gene

<1.->786

/gene="TNFSF5"

/locus\_tag="HCM5765"

ORIGIN

Query Match 67.8%; Score 463.6; DB 9; Length 786;

Best Local Similarity 99.1%; Pred. No. 2.2e-126;

Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGRAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259

Db 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 373

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGTGAAAAAAGGAT 319

Db 374 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGTGAAAAAAGGAT 433

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379

Db 434 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 493

QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439

Db 494 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 553

QY 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 499

Db 554 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCT 613

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT 559

Db 614 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGCGGGCAACAATCCATTCACT 673

QY 560 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619

Db 674 TGGGAGGAGTATTGGAATTGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAATC 669

Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAATC 783

RESULT 3

CD638712

LOCUS

DEFINITION AGENCOURT\_14532410 NIH\_MGC\_191 Homo sapiens cDNA clone IMAGE:30416146 5', mRNA sequence.

ACCESSION CD638712

VERSION CD638712.1 GI:31804800

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM215 row: h column: 11  
High quality sequence stop: 564.

FEATURES

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1. .767

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LOCUS	CN786611		
DEFINITION	CN786611.1	GI:47682100	
ACCESSION	CN786611		
VERSION	EST.		
KEYWORDS	Bos taurus (cow)		
SOURCE	Bos taurus		
ORGANISM	Bos taurus		
REFERENCE	1 (bases 1 to 628)		
AUTHORS	Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and Matukumalli,L.K.		
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Richard G. Baumann Bovine Functional Genomics Lab ANRI BLDG 162; BARC-EAST, Beltsville, MD 20705, USA Tel: 3015048604 Fax: 3015048744 Email: rbaumann@anri.barc.usda.gov Single pass sequencing. Bases called and trimmed with phred 0.00925 using options -trim_alt '' -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 18 Plate: 29 row: K column: 22 Seq primer: CCTATTTAGGTGACACTATAGAAC High quality sequence stop: 628.		
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	/clone_lib="BARC 8BOV"		
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Qy	478	CCCGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAATACCCACAGTTCGCCAAACCT	537
Db	129	CCAAGTGGATCAGAGAGAAATCTTACTGAGAGCTGCAAACACCCACAGTTCCTCCAAACCA	188
Qy	538	TGCGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTCTCGGTG	597
Db	189	TGCGGGCAGCAATCCATTCACTTAGGAGGAGTCTTTGAATTGCAATCGGGTCTTCGGTG	248
Qy	598	TTTGTCATGTGACTGATCCAAAGCCAAAGTGAGCCATGGCCTTGCGCTTCACGTCCTTTGGC	657
Db	249	TTTGTCATGTGACTGATCCAAAGTCAAGTGAGCCACGGGACGGGCTTCACATCATTTGGC	308
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Db	309	TTACTCAAACTC	320
RESULT 8			
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ACCESSION	CD640741		
VERSION	CD640741.1	GI:31808911	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 702)		
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDCM211 row: 1 column: 20 High quality sequence stop: 571.		
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ORIGIN									
CA). Note: this is a NIH_MGC Library."									
Query Match 32.2%; Score 220.2; DB 6; Length 702;									
Best Local Similarity 92.4%; Pred. No. 5.5e-54;									
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QY	260	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT	319						
Db	444	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGAT	503						
QY	320	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA	379						
Db	504	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA	563						
QY	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439						
Db	564	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	623						
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Db	624	GTCA--GCTCATTTATAGCCAGC	644						
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CD642064									
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DEFINITION									
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IMAGE:30418744 5', mRNA sequence.									
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ACCESSION									
VERSION									
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SOURCE									
ORGANISM									
Homo sapiens (human)									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 690)									
NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
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National Cancer Institute / NIH									
Bldg. 31 Rm10A07 Bethesda, MD 20892									
Email: cgapbs-r@mail.nih.gov									
Tissue Procurement: Narayan Bhat									
cDNA Library Preparation: CLONTECH Laboratories, Inc.									
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Agencourt Bioscience Corporation									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LLNL at:									
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Plate: NDCM222 row: d column: 17									
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Site 2: SfiI (ggccgcctcgcc); Library is oligo-dT primed									
and directionally cloned. PBMC - Peripheral Blood									
Mononuclear Cells. RNA was pooled from 3/6hour stimulation									
with PMA adn Ionomycin. 5' and 3' adaptors were used in									
cloning as follows: 5' adaptor sequence:									
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:									
5'-ATTCTAGAGCCGAGGGCCGACATG-DT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size 1.69									
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts									
by PCR. This library was enriched for full-length clones									
and was constructed by Clontech Laboratories (Palo Alto,									
CA). Note: this is a NIH_MGC Library."									
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Query Match 31.6%; Score 216; DB 6; Length 690;									
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Db	449	ATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGANAAGGAT	508						
QY	320	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA	379						
Db	509	ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAGCTGACCGTTAAAA	568						
QY	380	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTGTCCA	424						
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RESULT 10									
CD520208									
LOCUS									
DEFINITION									
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IMAGE:30412573 5', mRNA sequence.									
CD520208									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
Homo sapiens (human)									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 796)									
NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
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DNA Sequencing by: Agencourt Bioscience Corporation									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
Plate: NDCM206 row: c column: 14									
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Site 2: SfiI (ggccgcctcgcc); Library is oligo-dT primed									
and directionally cloned. PBMC - Peripheral Blood									
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5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:									
5'-ATTCTAGAGCCGAGGGCCGACATG-DT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size 1.69									
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by PCR. This library was enriched for full-length clones									
and was constructed by Clontech Laboratories (Palo Alto,									
CA). Note: this is a NIH_MGC Library."									
ORIGIN									
Query Match 31.6%; Score 216; DB 6; Length 690;									
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IMAGE:30412573 5', mRNA sequence.									
CD520208									
ACCESSION									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 796)									
NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
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5'-ATTCTAGAGCCGAGGGCCGACATG-DT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size 1.69									
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts									
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ORIGIN									
Query Match 31.6%; Score 216; DB 6; Length 690;									
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IMAGE:30412573 5', mRNA sequence.									
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ACCESSION									
VERSION									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
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Site 2: SfiI (ggccgcctcgcc); Library is oligo-dT primed									
and directionally cloned. PBMC - Peripheral Blood									
Mononuclear Cells. RNA was pooled from 3/6hour stimulation									
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cloning as follows: 5' adaptor sequence:									
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C, or G and N = A, C, G, or T). Average insert size 1.69									
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts									
by PCR. This library was enriched for full-length clones									
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ORIGIN									
Query Match 31.6%; Score 216; DB 6; Length 690;									
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IMAGE:30412573 5', mRNA sequence.									
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ACCESSION									
VERSION									
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NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
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http://image.llnl.gov									
Plate: NDCM206 row: c column: 14									
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/lab_host="DH10B (T1 phage-resistant)"									
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Site 2: SfiI (ggccgcctcgcc); Library is oligo-dT primed									
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5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:									
5'-ATTCTAGAGCCGAGGGCCGACATG-DT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size 1.69									
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by PCR. This library was enriched for full-length clones									
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Query Match 31.6%; Score 216; DB 6; Length 690;									
Best Local Similarity 97.3%; Pred. No. 9.7e-53;									
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QY	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC	259						
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DEFINITION									
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IMAGE:30412573 5', mRNA sequence.									
CD520208									
ACCESSION									
VERSION									
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
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Site 2: SfiI (ggccgcctcgcc); Library is oligo-dT primed									
and directionally cloned. PBMC - Peripheral Blood									
Mononuclear Cells. RNA was pooled from 3/6hour stimulation									
with PMA adn Ionomycin. 5' and 3' adaptors were used in									
cloning as follows: 5' adaptor sequence:									
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:									
5'-ATTCTAGAGCCGAGGGCCGACATG-DT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size 1.69									
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts									
by PCR. This library was enriched for full-length clones									
and was constructed by Clontech Laboratories (Palo Alto,									
CA). Note: this is a NIH_MGC Library."									
ORIGIN									
Query Match 31.									









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